

GenCore version 5.1.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 14:52:22 ; Search time 196 Seconds  
(without alignments)  
335.914 Million cell updates/sec

Title: US-10-614-481-9

Perfect score: 759

Sequence: 1 MWLQNLGLLTGVVSNPAPT.....KNLKDFLFEIPDCWKPAQK 144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	759	100.0	144	4 ABP98711	Abp98711 Equine gr
2	759	100.0	144	4 AAB37147	Aab37147 Equine gr
3	641	84.5	144	2 AAR23662	Aar23662 Ovine GM-
4	587	77.3	144	2 AAR54818	Aar54818 CHEF-2. 3
5	586	77.2	144	1 AAP60418	Aap60418 Human gra
6	586	77.2	144	1 AAP70657	Aap70657 Sequence
7	586	77.2	144	2 AAR04098	Aar04098 Metapycoc
8	586	77.2	144	2 AAR71118	Aar71118 GM-CSF en
9	586	77.2	144	2 AAR92800	Aar92800 Human GM-
10	586	77.2	144	2 AAW60031	Aaw60031 Human gra
11	586	77.2	144	3 AAB18633	Aab18633 Amino aci
12	586	77.2	144	4 AAB50871	Aab50871 Human GM-
13	586	77.2	144	4 AAB84602	Aab84602 Amino aci
14	586	77.2	144	5 ABB05055	Abb05055 Human gra
15	586	77.2	144	5 AAU11977	Aau11977 Human GM-
16	586	77.2	144	6 ABR55847	Abr55847 Human GM-
17	586	77.2	144	7 AAE14938	Aae14938 Human gra
18	586	77.2	144	7 ADF15243	Adf15243 Human alb
19	586	77.2	144	7 ADF15149	Adf15149 Human alb
20	586	77.2	144	7 ADF15242	Adf15242 Human alb
21	586	77.2	144	7 ADF15150	Adf15150 Human alb
22	586	77.2	144	7 ADH44684	Adh44684 Human GM-
23	586	77.2	144	7 ADI01020	Adi01020 Human gra

24	586	77.2	144	8 ADH10509	Adh10509 Human GM-
25	586	77.2	144	8 ADL66118	Adl66118 Human gra
26	586	77.2	144	8 ADL66120	Adl66120 Human PAP
27	586	77.2	144	8 ADL16730	Adl16730 Human gra
28	586	77.2	144	8 ADN07713	Adn07713 Human G-C
29	586	77.2	144	8 ADN49690	Adn49690 Human gra
30	586	77.2	144	8 ADP12451	Adp12451 Protein e
31	586	77.2	144	8 ADP19843	Adp19843 Human GMC
32	586	77.2	144	8 ADO59665	Ado59665 Human GMC
33	586	77.2	144	8 ADR46068	Adr46068 Human gra
34	586	77.2	144	8 ADR46066	Adr46066 Human gra
35	586	77.2	144	8 ADS88047	Ads88047 Tumour tr
36	586	77.2	144	8 ADU74366	Adu74366 Human gra
37	586	77.2	144	9 ADV96467	Adv96467 Human GM-
38	586	77.2	144	9 ADY19524	Ady19524 PRO polyp
39	586	77.2	144	9 ADY16395	Ady16395 PRO polyp
40	586	77.2	144	9 ADY84980	Ady84980 Human gra
41	586	77.2	144	9 ADZ26537	Adz26537 Human GMS
42	586	77.2	144	9 ADY99886	Ady99886 Human imm
43	586	77.2	144	9 ADZ20507	Adz20507 Human gra
44	586	77.2	144	9 AEB10855	Aeb10855 Human GM-
45	586	77.2	144	9 AEB54698	Aeb54698 Human col

#### ALIGNMENTS

#### RESULT 1

ID ABP98711 standard; protein; 144 AA.

XX ABP98711;

DT 27-JUN-2003 (first entry)

DE Equine granulocyte-macrophage colony stimulating factor.

XX Granulocyte-macrophage colony stimulating factor; GM-CSF; antibacterial;  
KW antiviral; vaccine; animal; immunogen; DMRIE; cationic lipid; dog; cat;  
KW quaternary ammonium salt; canine distemper virus; canine herpes virus;  
KW canine parainfluenza virus; feline herpes virus; equine herpes virus;  
KW horse.

XX Equus caballus.

XX WO200077043-A2.

XX 21-DEC-2000.

XX 08-JUN-2000; 2000WO-FR001592.

XX 10-JUN-1999; 99FR-00007604.

XX 19-JUL-1999; 99US-0144490P.

XX (MERI-) MERIAL.

XX Fischer LJ, Barzu-Le Roux S, Audonnet JF;

XX WPI; 2001-071259/08.

XX N-PSDB; ABZ80828.

XX DNA vaccine containing plasmid and cationic lipid containing quaternary ammonium salt, useful for protecting pets and sports animals against, e.g. herpes virus.

XX Example 10; Fig 26; 109pp; French.

XX The invention relates to a novel DNA vaccine against pathogens that affect pets and sports animals comprises a plasmid containing a sequence, expressible in vivo, that encodes an immunogen from the relevant pathogen and a cationic lipid containing a quaternary ammonium salt, particularly N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium (DMRIE). The immunogens are particularly taken from canine distemper

CC virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes  
CC virus (CHV), feline herpes virus type 1 (FHV-1), equine herpes virus type  
CC 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of  
CC an immunogenic stimulation factor especially a granulocyte-macrophage  
CC colony stimulation factor (GM-CSF) to enhance the immunogenic response.  
CC The vaccines, which may be multivalent, are particularly used to protect  
CC dogs, cats and horses against bacterial and viral diseases, particularly  
CC those caused by the Paramyxoviridae. Formulations with the quaternary  
CC ammonium salt provide a better immune response and thus more efficient  
CC protection, particularly when administered subcutaneously. This sequence  
CC represents an equine GM-CSF used in the invention

XX SQ Sequence 144 AA;  
Query Match 100.0%; Score 759; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 2.4e-74;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLQNLGLLVVYSMPAPTRQPSVTPRPQHVDAIKEALSLLNNSDPTAAIMNETVEV 60  
DB 1 MWLQNLGLLVVYSMPAPTRQPSVTPRPQHVDAIKEALSLLNNSDPTAAIMNETVEV 60  
QY 61 SETFDAEELTCLQTRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120  
DB 61 SETFDAEELTCLQTRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120  
QY 121 KSFKKNLKDPLFEIPFDCWKPAQK 144  
DB 121 KSFKKNLKDPLFEIPFDCWKPAQK 144

RESULT 2  
AAB37147  
ID AAB37147 standard; protein; 144 AA.  
XX AAB37147;  
XX 18-JUN-2002 (first entry)  
XX Equine granulocyte-macrophage colony stimulating factor.  
DE Immunostimulatory; granulocyte-macrophage colony stimulating factor;  
KW horse; reverse transcriptase PCR; colony formation; blood; cytotoxicity;  
KW inflammation; vector; adjuvant; immunogen; vaccination; vaccine;  
KW equine herpes; tetanus; Borrelia burgdorferi; rabies.  
XX  
OS Equus sp.  
XX  
XX WO200077210-A1.  
XX  
XX 21-DEC-2000.  
XX  
XX 08-JUN-2000; 2000WO-FR001590.  
XX  
XX 10-JUN-1999; 99US-0138843P.  
XX  
XX (MERI-) MERIAL.  
XX  
XX Bublot M, Perez JM, Andreoni CMP;  
XX  
XX WPI; 2001-080689/09.  
XX  
XX N-PSDB; AAF28953.  
XX  
XX Novel DNA encoding equine granulocyte-macrophage colony-stimulating  
XX factor, useful as adjuvant for vaccines and as non-specific  
XX immunostimulant.  
XX  
XX Claim 6; Fig 1; 34pp; French.  
XX

CC This sequence represents a horse granulocyte-macrophage colony  
CC stimulating factor (GM-CSF). The corresponding gene was isolated from  
CC horse lymphocytes using a reverse transcriptase PCR method with primers  
CC AAF28954-AAF28960. The protein has been shown to have at least 75%

CC homology with GM-CSF proteins from other animal species. GM-CSF induces  
CC colony formation in various types of blood cells and particularly induces  
CC cytotoxicity of macrophages; stimulates antibody-dependent cytotoxicity,  
CC and causes recruitment of leucocytes to sites of inflammation. Vectors  
CC containing the gene or the protein itself, are useful as adjuvants in  
CC immunogenic or vaccinating compositions for horses, e.g. for protection  
CC against equine herpes, tetanus, Borrelia burgdorferi, rabies etc. Also as  
CC non-specific stimulators of the immune system. In a specific example,  
CC plasmid p0P097, containing the sequence for equine GM-CSF was used to  
CC transform CHO-K1 cells and the transformants grown for 48 hours. The  
CC culture supernatant was then added to culture medium being used to grow  
CC porcine bone marrow cells. After 14 days, the mean number of colonies per  
CC culture box was 12-15, compared with none for cells grown in absence of  
CC GM-CSF. Equine GM-CSF allows a reduction in the amount of  
CC immunogenic/vaccinating component required, and may induce a response in  
CC animals that would otherwise be non-responders

XX SQ Sequence 144 AA;

Query Match 100.0%; Score 759; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 2.4e-74;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLQNLGLLVVYSMPAPTRQPSVTPRPQHVDAIKEALSLLNNSDPTAAIMNETVEV 60  
DB 1 MWLQNLGLLVVYSMPAPTRQPSVTPRPQHVDAIKEALSLLNNSDPTAAIMNETVEV 60  
QY 61 SETFDAEELTCLQTRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120  
DB 61 SETFDAEELTCLQTRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120  
QY 121 KSFKKNLKDPLFEIPFDCWKPAQK 144  
DB 121 KSFKKNLKDPLFEIPFDCWKPAQK 144

RESULT 3  
AAR23662  
ID AAR23662 standard; protein; 144 AA.  
XX AAR23662;  
XX 25-MAR-2003 (revised)  
DT 27-OCT-1992 (first entry)  
XX  
DE Ovine GM-CSF.  
XX  
XX Granulocyte-macrophage colony-stimulating factor; immuno-depression;  
KW vaccine adjuvants; cytokine.  
XX  
OS Ovis aries.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..17  
FT Peptide /note= "putative signal sequence"  
FT Peptide 18..144  
FT Peptide /note= "mature protein"  
XX  
XX WO2005255-A.  
XX  
XX 02-APR-1992.  
XX  
XX 13-SEP-1990; 90AU-00002294.  
XX  
XX 13-SEP-1990; 90AU-00002294.  
PR 21-MAR-1991; 91AU-00005175.  
XX  
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
XX Wood PR, Rothel JS, Seow HF;  
XX WPI; 1992-150483/18.  
DR N-PSDB; AAQ24294.  
DR

XX DNA encoding ovine cytokine(s) - used to prepare recombinant cytokine(s)  
 PT for treatment of immuno-depression in sheep.  
 XX Disclosure; Fig 3; 79pp; English.

XX The sequence is that of the ovine granulocyte-macrophage colony  
 CC stimulating factor (GM-CSF), a cytokine-like molecule. The ovine  
 CC cytokines will be useful in the intensive livestock industries such as  
 CC live animal export trade, feed-lots and intensive rearing industries,  
 CC where animals are subjected to great environmental challenge with  
 CC infectious diseases, partic. respiratory infections, and are more prone  
 CC to immunodepressive effects. The cytokines may be used for treatment or  
 CC prophylaxis to maintain, stimulate or enhance immunoresponsiveness. They  
 CC may also be useful as natural adjuvants for vaccines for sheep and  
 CC cattle. See also AAR23661-R23667. (Updated on 25-MAR-2003 to correct PA  
 CC field.)

XX Sequence 144 AA;  
 SQ Query Match 84.5%; Score 641; DB 2; Length 144;  
 Best Local Similarity 84.0%; Pred. No. 1.8e-61;  
 Matches 121; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 MWLQNLGLLVVYMPAPTRQPSVTRPQHVDAIKEALSLNNSDAAIMNETVEV 60  
 Db 1 MWLQNLGLLVVYMPAPTRQPSVTRPQHVDAIKEALSLNNSDAAIMNETVEV 60

QY 61 SETFAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTF 120  
 Db 61 SEMFDSQPTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTF 120

QY 121 KSFKNLKDLFLFEIPDFCWKPAQK 144  
 Db 121 KSFKNLKDLFLFEIPDFCWKPAQK 144

RESULT 4  
 AAR54818  
 ID AAR54818 standard; protein; 144 AA.  
 AC AAR54818;  
 DT 25-MAR-2003 (revised)  
 DT 10-MAR-2003 (revised)  
 DT 07-NOV-1994 (first entry)  
 XX CHEF-2.  
 XX Cytokine; chimerism enhancing factors; porcine; transplant;  
 KW xenogeneic cells; bone marrow; African swine fever; Hog cholera;  
 KW Pseudorabies.  
 XX Sus scrofa.  
 XX Key Location/Qualifiers  
 FT Peptide 1..17  
 FT /note= "signal peptide"  
 XX WO9409803-A1.  
 XX 11-MAY-1994.  
 XX 26-OCT-1993; 93WO-US010295.  
 XX 27-OCT-1992; 92US-00967188.  
 PR 08-OCT-1993; 93US-00133979.  
 XX (BIOT-) BIOTRANSPLANT INC.  
 XX Ponath PD, Rosa MD, Monroy RL, Schacter BZ, Hawley RJ;  
 XX WPI; 1994-167114/20.

DR N-PSDB; AAQ64864.  
 XX Porcine cytokine Chimerism Enhancing Factors (CHEFs) and DNA - used to  
 PT enhance xenograft tolerance.  
 XX Claim 25; Page 72; 113pp; English.

XX The sequence is that of a porcine cytokine designated chimerism enhancing  
 CC factor (CHEF-2). The cytokine can be used for improving engraftment,  
 CC stabilisation and proliferation of tissues, esp. bone marrow cells, in  
 CC xenogeneic transplantation. The cytokine may be used to prevent or treat  
 CC various swine diseases, e.g. African swine fever, Hog cholera,  
 CC Pseudorabies, etc. See also AAR54817-9. (Updated on 10-MAR-2003 to add  
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 144 AA;  
 SQ Query Match 77.3%; Score 587; DB 2; Length 144;  
 Best Local Similarity 76.4%; Pred. No. 1.4e-55;  
 Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 MWLQNLGLLVVYMPAPTRQPSVTRPQHVDAIKEALSLNNSDAAIMNETVEV 60  
 Db 1 MWLQNLGLLVVYMPAPTRQPSVTRPQHVDAIKEALSLNNSDAAIMNETVEV 60

QY 61 SETFAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTF 120  
 Db 61 CEMFDPQPTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTF 120

QY 121 KSFKNLKDLFLFEIPDFCWKPAQK 144  
 Db 121 KSFKNLKDLFLFEIPDFCWKPAQK 144

RESULT 5  
 AAP60418  
 ID AAP60418 standard; protein; 144 AA.  
 AC AAP60418;  
 DT 25-MAR-2003 (revised)  
 DT 01-JAN-1980 (first entry)  
 XX Human granulocyte macrophage-colony stimulating factor.  
 DE Granulocyte; macrophage; colony stimulating factor; chemotherapy;  
 KW neoplastic disease therapy; infectious disease therapy; ss.  
 XX Homo sapiens.  
 XX WO8603225-A.  
 XX 05-JUN-1986.  
 XX 18-NOV-1985; 85WO-US002250.  
 PR 20-NOV-1984; 84US-00673898.  
 XX (SCHE) SCHERING BIOTECH CORP.  
 XX Yokota T, Lee FD, Rennick D, Arai K;  
 XX WPI; 1986-155831/24.  
 DR N-PSDB; AAN60364.  
 XX New poly:peptide(s) for colony stimulation of granulocytes - useful for  
 PT enhancing body defences against neoplasms and infectious diseases and to  
 PT overcome myelo:suppression in chemotherapy.  
 XX Disclosure; Fig 1; 53pp; English.  
 XX The protein has GM-CSF activity and is useful in elucidating control  
 CC mechanisms of mammalian immune responses. It is also useful for

CC administration to enhance natural defences against neoplastic and  
CC infectious diseases or as an adjunct in chemotherapy to overcome  
CC myelosuppression. GM-CSF is prepared by conventional recombinant DNA  
CC techniques. The factor has activity on human neutrophilic granulocytes,  
CC macrophages and eosinophils. (Updated on 25-MAR-2003 to correct PF  
CC field.) (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 144 AA;

Query Match 77.2%; Score 586; DB 1; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.8e-55;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLNQLLLGLTGVVSMPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60  
Db 1 MWLQSLLLGLTVACISAPARSPSPSTQWHEVNAIQEARLLNLSRDTAAEMNETVEI 60

Qy 61 SETFDAELTCLQRLKLYKQGLRSLIKLGGPLTMMASHYKHQCHPPTLETSCATQMITF 120  
Db 61 SEMFDLQEBPTCLQRLKLYKQGLRSLIKLGGPLTMMASHYKHQCHPPTLETSCATQIITF 120

Qy 121 KSFKNLKDFLFEIPFDCWKPAQK 144  
Db 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 6  
AAP70657  
ID AAP7065; utandard; protein; 144 AA.  
AC AAP7065';  
XX  
XX  
DT 18-APR-1991 (first entry)  
DE  
DE Sequencu of a human granulocyte-macrophage colony stimulating factor (hGM  
DE -CSF)-like polypeptide isolated from 5637 cell line.  
XX  
KW AIDS thirapy; leukocyte; leucaemia.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Cleavage-site 17..18  
FT /note= "for signal peptide"  
XX  
XX  
FN W08702060-A.  
PD 09-APR-1987.  
XX  
PF 03-OCT-1986; 86WO-US002106.  
XX  
PR 03-OCT-1985; 85US-00783414.  
XX  
PA (BIOJ ) BIOGEN NV.  
PA (DELA/) DELAMARTER J.  
XX  
XX Delamarter J, Ernst JF;  
XX  
XX WPI; 1987-108701/15.  
DR N-PSDB; AAN71002.  
XX  
XX Human granulocyte-macrophage stimulating factor-like polypeptide(s) -  
PT produced from recombinant DNA sequence having 5' terminal alteration.  
XX  
XX Example; Fig 2; 61pp; English.  
XX  
XX A recombinant DNA molecule encoding a hGM-CSF is claimed wherein there is  
CC a 5' terminal alteration allowing higher yield than the native DNA  
CC sequence. The cpds. may be used to reduce the likelihood of infections in  
CC immunologically compromised individuals, such as those suffering from  
CC AIDS by increasing their white blood cell count  
XX  
XX Sequence 144 AA;

Query Match 77.2%; Score 586; DB 1; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.8e-55;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLNQLLLGLTGVVSMPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60  
Db 1 MWLQSLLLGLTVACISAPARSPSPSTQWHEVNAIQEARLLNLSRDTAAEMNETVEI 60

Qy 61 SETFDAELTCLQRLKLYKQGLRSLIKLGGPLTMMASHYKHQCHPPTLETSCATQMITF 120  
Db 61 SEMFDLQEBPTCLQRLKLYKQGLRSLIKLGGPLTMMASHYKHQCHPPTLETSCATQIITF 120

Qy 121 KSFKNLKDFLFEIPFDCWKPAQK 144  
Db 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 7  
AAR04098  
ID AAR04098 standard; protein; 144 AA.  
XX  
AC AAR04098;  
XX  
DT 10-SEP-1990 (first entry)  
XX  
DE Metapyrocatechase gene product.  
XX  
KW Metapyrocatechase; GM-CSF; leukopaenia; osteomyelodysplasia;  
KW granulocyte macrophage colony stimulating factor; ds.  
XX  
OS Homo sapiens.  
XX  
PN JP02076596-A.  
XX  
PD 15-MAR-1990.  
XX  
PF 13-SEP-1988; 88JP-00229468.  
XX  
PR 13-SEP-1988; 88JP-00229468.  
XX  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
XX  
XX WPI; 1990-128250/17.  
DR N-PSDB; AAQ04017.  
XX  
PT Human granulocyte macrophage colony stimulating factor derivs. - useful  
PT for treating diseases due to leukopenia or osteomyelo-dysplastic.  
XX  
PS Disclosure; Page ?; -pp; Japanese.  
XX  
CC Human GM-CSF derivs. have polypeptide fragment from N-terminal of  
CC metapyrocatechase, bonded at its C-terminal to the N-terminal of GM-CSF.  
CC Expression vectors pMGMI and pMGM3 also contain the tac promoter/operator  
CC and the SD sequence of metapyrocatechase  
XX  
SQ Sequence 144 AA;

Query Match 77.2%; Score 586; DB 2; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.8e-55;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLNQLLLGLTGVVSMPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60  
Db 1 MWLQSLLLGLTVACISAPARSPSPSTQWHEVNAIQEARLLNLSRDTAAEMNETVEI 60

Qy 61 SETFDAELTCLQRLKLYKQGLRSLIKLGGPLTMMASHYKHQCHPPTLETSCATQMITF 120  
Db 61 SEMFDLQEBPTCLQRLKLYKQGLRSLIKLGGPLTMMASHYKHQCHPPTLETSCATQIITF 120

Qy 121 KSFKNLKDFLFEIPFDCWKPAQK 144  
Db 121 ESFKENLKDFLLVIPFDCWEPVQE 144





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XX AC AAW60031;
XX 18-AUG-1998 (first entry)
XX Human granulocyte macrophage colony stimulating factor (GM-CSF).
XX Recombinant poxvirus; biological response modifier; IL-12; GM-CSF;
KW granulocyte macrophage colony stimulating factor; prevention; tumour;
KW interleukin; cytokine; treatment.
XX OS Homo sapiens.
XX WO9815635-A2.
XX 16-APR-1998.
XX 03-OCT-1997; 97WO-CA000729.
XX 04-OCT-1996; 96US-0027530P.
XX (CONN-) CONNAUGHT LAB LTD.
XX (VIRO-) VIROGENETICS CORP.
XX Gajewczyk DM, Tartaglia J, Cox B, Alexander J, Bonnet MC, Diaz I;
PI Cornet H, Paoletti E, Klein MH;
XX WPI; 1998-240821/21.
XX N-PSDB; AAV29700.
XX Recombinant poxvirus encoding biological response modifier - useful for
PT the treatment or prevention of tumours.
XX Disclosure; Fig 9A-F; 52pp; English.
XX This represents the human granulocyte macrophage colony stimulating
CC factor (GM-CSF). A murine GM-CSF which is similar to the human GM-CSF is
CC used for generating a recombinant poxvirus. The recombinant poxvirus
CC comprises a nucleic acid sequence encoding a biological response modifier
CC or its immunomodulating fragment in a non-essential region of the
CC recombinant virus genome. The biological response modifier may be a
CC cytokine, e.g. interleukin-12 (IL-12), IL-2 or GM-CSF. The recombinant
CC poxvirus is used to transfect cells for expression of the biological
CC response modifier. The products are useful for the treatment of tumours
CC or for protecting a host against tumour formation
XX Sequence 144 AA;
XX Query Match 77.2%; Score 586; DB 2; Length 144;
XX Best Local Similarity 76.4%; Pred. No. 1.8e-55;
XX Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
QY 1 MWLQNLGTVVYVSMPTPTROPSPVTRPQWHDVDAIKALSLLNNSSDTAAMNETVEV 60
DB 1 MWLQNLGTVVYVSMPTPTROPSPVTRPQWHDVDAIKALSLLNNSSDTAAMNETVEV 60
QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
QY 121 KSFKNLKDFLFEIPDCWKPAQK 144
DB 121 ESFKENLKDFLLVIPDFCWEVPQK 144
RESULT 11
AAB18633
ID AAB18633 standard; protein; 144 AA.
XX AAB18633;
XX 22-JAN-2001 (first entry)
XX

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```

DE Amino acid sequence of a human GMCSF protein helix A fragment.
XX zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour; GMCSF.
XX OS Homo sapiens.
XX WO200053761-A2.
XX 14-SEP-2000.
XX 09-MAR-2000; 2000WO-US006067.
XX 09-MAR-1999; 99US-00264908.
XX 11-MAR-1999; 99US-00265992.
XX 01-JUL-1999; 99US-0142013P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AU, Dillon SR, Hammond AK;
XX WPI; 2000-565600/52.
XX New human cytokine, designated zalphall ligand, useful for stimulating
PT the proliferation and/or development of hematopoietic cells in vitro and
PT in vivo, and for treating tumorigenesis.
XX Claim 10; Page 254; 256pp; English.
XX The present sequence represents part of a human GMCSF protein. It is used
CC to produce fusion proteins with a human zalphall ligand. Zalphall ligand
CC is a cytokine. The zalphall ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
CC for cloning the zalphall gene. The zalphall ligand is useful for treating
CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for
CC treating leukaemias and lymphomas. Antagonists against zalphall ligand
CC are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect
XX Sequence 144 AA;
XX Query Match 77.2%; Score 586; DB 3; Length 144;
XX Best Local Similarity 76.4%; Pred. No. 1.8e-55;
XX Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
QY 1 MWLQNLGTVVYVSMPTPTROPSPVTRPQWHDVDAIKALSLLNNSSDTAAMNETVEV 60
DB 1 MWLQNLGTVVYVSMPTPTROPSPVTRPQWHDVDAIKALSLLNNSSDTAAMNETVEV 60
QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
QY 121 KSFKNLKDFLFEIPDCWKPAQK 144
DB 121 ESFKENLKDFLLVIPDFCWEVPQK 144
RESULT 12
AAB50871
ID AAB50871 standard; protein; 144 AA.
XX AAB50871;
XX

```

19-MAR-2001 (first entry)  
Human GM-CSF.  
Human; zalpha31; alpha helical protein-31;  
granulocyte-macrophage colony stimulating factor; GM-CSF; cytostatic;  
antiinflammatory; antiarthritic; antirheumatoid; immunosuppressive;  
antiaschmatic; antibacterial; osteopathic; antiatherosclerotic;  
antipsoriatic; dermatological; anti-HIV; gene therapy; osteoporosis;  
Paget's disease; hyperparathyroidism; acute pancreatitis;  
gastrointestinal disorder; inflammation; heart disorder; viral infection.  
Homo sapiens.  
WO200073458-A1.  
07-DEC-2000.  
26-MAY-2000; 2000WO-US014795.  
28-MAY-1999; 99US-0136485P.  
(ZMO ) ZYMOGENETICS INC.  
Conklin DC;  
WPI; 2001-070967/08.  
Novel 4-helix bundle cytokine, Zalpha31, useful for regulating the  
function of immune system and for treating thyroid, adrenal, lymphoid,  
inflammatory, pancreatic, blood or bone disorders.  
Disclosure; Page 107-108; 111pp; English.  
The present sequence is given in a specification relating to  
polynucleotide and polypeptide molecules for mammalian secreted alpha  
helical protein-31 (zalpha31). The polypeptides are a novel four-helix  
bundle cytokine and may be used to regulate the functioning of the immune  
system. The polypeptides are used to identify and isolate receptors  
involved in spermatogenesis, steroidogenesis, testicular differentiation  
and regulatory control of the hypothalamic-pituitary gonadal axis,  
thyroid, heart and adrenal function. They are useful for treating  
disorders of the reproductive system, thyroid, adrenal, heart and  
immunological systems. Zalpha31 polypeptides, or antagonists are useful  
in the treatment of e.g. osteoporosis, Paget's disease, and  
hyperparathyroidism, acute pancreatitis and gastrointestinal disorders  
and as analgesics, especially for bone pain. They can be used to treat  
atherosclerosis, pelvic inflammatory disease, (PID), psoriasis,  
arthritis, eczema, scleroderma and other inflammatory diseases. The  
polypeptides, nucleic acids and/or antibodies can be used to treat heart  
disorders. They can limit infarct size following a heart attack, aid in  
recovery after heart transplantation, treat complications related to poor  
circulation e.g. diabetic foot ulcers, treat stroke, improve cardiac  
function, induce skeletal muscle neogenesis and/or hyperplasia, be used  
in kidney regeneration and/or for treating systemic and pulmonary  
hypertension. Zalpha31 can be used for treating viral leukemias,  
acquired immunodeficiency syndrome (AIDS) or gastrointestinal viral  
infections  
Sequence 144 AA;  
Query Match 77.2%; Score 586; DB 4; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.8e-55;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
1 MWLQNLGTVVYVSMPTPTQPSVTPRQWHDVAIKKALSLLNNSDPTAAIMNETVEVY 60  
1 MWLQNLGTVVYVSMPTPTQPSVTPRQWHDVAIKKALSLLNNSDPTAAIMNETVEVY 60  
61 SETFDABELTCLQTRLYKQGLRSLIKLEGPLTWMASHYKQHCPTLETSCATQMTTF 120  
61 SEMFDLQEPCLQTRLYKQGLRSLIKLEGPLTWMASHYKQHCPTLETSCATQMTTF 120

121 KSFKKNLKDFLFEIPDFDCWKPAQK 144  
:|||||:|||||:|  
121 ESFKENLKDFLLVIPDFCWEVQVE 144  
:|||||:|||||:|  
RESULT 13  
AAB84602  
ID AAB84602 standard; protein; 144 AA.  
XX AAB84602;  
AC AAB84602;  
XX 05-SEP-2001 (first entry)  
XX Amino acid sequence of granulocyte macrophage colony stimulating factor.  
XX Growth factor; protein inhibitor; protease; damaged tissue;  
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;  
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;  
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;  
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;  
KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;  
KW vascular endothelial growth factor; urokinase plasminogen activator;  
KW dermal ulcer; wound.  
XX Homo sapiens.  
XX OS  
XX WO200149309-A2.  
XX 12-JUL-2001.  
XX 21-DEC-2000; 2000WO-IB001935.  
XX 29-DEC-1999; 99GB-00030768.  
XX (PFIZ ) PFIZER LTD.  
XX (PFIZ ) PFIZER INC.  
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;  
XX WPI; 2001-418351/44.  
XX N-PSDB; AAH28217.  
XX Composition for the treatment of damaged tissue i.e. chronic wounds and  
dermal ulcers comprises an inhibitor agent i.e. a protease and a growth  
factor.  
XX Disclosure; Page 548; 572pp; English.  
XX The specification describes a pharmaceutical composition, comprising a  
growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent  
inhibits the action of at least one specific adverse protein, i.e. a  
protease, that is upregulated in a damaged tissue such as a wound  
environment. Growth factors which are included in the composition of the  
invention are platelet-derived growth factor (PDGF), fibroblast growth  
factor (FGF), connective tissue derived growth factor (CTGF),  
keratinocyte-derived growth factor (KGF), transforming growth factor-beta  
(TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),  
epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),  
and chrysalin. Inhibitors which are included in the composition of the  
invention include inhibitors of urokinase-type plasminogen activator  
(uPA) and matrix metalloproteinase (MMP). The composition is useful for  
the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.  
XX The present sequence represents a human GM-CSF, and is used to produce  
XX the composition of the invention  
XX Sequence 144 AA;  
Query Match 77.2%; Score 586; DB 4; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.8e-55;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
1 MWLQNLGTVVYVSMPTPTQPSVTPRQWHDVAIKKALSLLNNSDPTAAIMNETVEVY 60  
:|||||:|||||:|





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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 14:56:07 ; Search time 39 Seconds  
(without alignments)  
355.262 Million cell updates/sec

Title: US-10-614-481-9  
Perfect score: 759  
Sequence: 1 MWLQNLLLLGTWVYVSMAPT.....KNLKDFLFEIPDCWKPAQK 144

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	641	84.5	144	1 A61632	granulocyte-macrop
2	637	83.9	144	2 JH0469	granulocyte-macrop
3	586	77.2	144	1 FQHUGM	granulocyte-macrop
4	574.5	75.7	143	1 FQBOGM	granulocyte-macrop
5	566	74.6	144	2 A44936	granulocyte-macrop
6	450.5	59.4	153	1 FQMSGM	granulocyte-macrop
7	448	59.0	127	2 I46269	granulocyte-macrop
8	84.5	11.1	660	2 T39964	hypothetical coile
9	81.5	10.7	424	2 F69476	acetylornithine am
10	79.5	10.5	913	1 B42543	DNA-directed DNA p
11	78.5	10.3	397	2 F97707	acyl-CoA desaturas
12	78.5	10.3	400	2 G90465	acyl-CoA dehydroge
13	78.5	10.3	760	2 S70294	FUN21 protein - ye
14	78.5	10.3	943	2 E84429	probable receptor-
15	77	10.1	490	2 A96556	probable tRNA-guan
16	77	10.1	913	2 F86833	phage infection pr
17	76.5	10.1	901	2 T17675	DNA-directed DNA p
18	76	10.0	311	2 G86383	probable mitochond
19	76	10.0	560	2 S48724	hexose transport p
20	75	9.9	389	2 S53612	gene MSP-2 protei
21	74.5	9.8	1276	2 T18526	SREBP cleavage act
22	74	9.7	1607	2 T03022	MAP kinase kinase
23	73.5	9.7	187	2 B83695	hypothetical prote
24	73.5	9.7	193	2 G83901	hypothetical prote
25	73	9.6	901	2 A48653	phage infection pr
26	72.5	9.6	394	2 S36512	E2 protein - human
27	72.5	9.6	474	2 T20706	hypothetical prote
28	72.5	9.6	674	2 S75662	sensory transducti
29	72.5	9.6	913	1 A42543	DNA-directed DNA p

30 9.5 167 2 F84559 histone H1 [import  
31 72 187 2 H81979 hypothetical prote  
32 72 884 2 B96492 probable polypeptide  
33 72 1127 2 T30334 AND-1 protein - AF  
34 72 1364 2 T10236 xanthine dehydroge  
35 72 1450 2 T30273 hypothetical prote  
36 71 9.4 208 2 JS0512 fusaric acid resis  
37 71 9.4 312 2 G87536 acetolactate synth  
38 71 9.4 591 2 F64334 helix-loop-helix p  
39 71 9.4 644 2 A42220 mismatch repair pr  
40 71 9.4 769 2 S54525 DNA mismatch repai  
41 71 9.4 828 2 D81522 DNA mismatch repai  
42 71 9.4 828 2 C86608 DNA mismatch repai  
43 71 9.4 828 2 G72017 probable chitinase  
44 71 9.4 1088 2 D82246 myosin VII-like pr  
45 71 9.4 2121 2 A59233

ALIGNMENTS

RESULT 1

A61632

granulocyte-macrophage colony-stimulating factor precursor - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: A61632

R:O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.

Immunol. Cell Biol. 69, 51-55, 1991

A:Title: Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stim

A:Reference number: A61632; MUID:91331592; PMID:1869289

A:Accession: A61632

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-144 <OAB>

A:Cross-references: UNIPROT:Q9MYK4; UNIPARC:UPI000008836D; GB:X55991; NID:G6983759; PIDN

C:Superfamily: granulocyte-macrophage colony-stimulating factor

F:1-17/Domain: signal sequence #status predicted <SIG>

Query Match 84.5%; Score 641; DB 1; Length 144;

Best Local Similarity 84.0%; Pred. No. 3.9e-54; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MWLQNLLLLGTWVYVSMAPTROPSPVTRPQHQVDAIKEALSLNNSSDTAAIMNETVEV 60

Db 1 MWLQNLLLLGTWVYVSMAPTROPSPVTRPQHQVDAIKEALSLNNSSDTAAIMNETVEV 60

Qy 61 SETFDABELTCLQRLKLYKQGLRGLSLKLEGLPTMMASHYKQHCPTTLETSCATQMTIF 120

Db 61 SEMFDSQEPTECLQRLKLYKQGLRGLSLTSLTGLTMMASHYKQHCPTTLETSCATQMTIF 120

Qy 121 KSFKKNLKDFLFEIPDCWKPAQK 144

Db 121 KSFKKNLKDFLFEIPDCWKPAQK 144

RESULT 2

JH0469

granulocyte-macrophage colony-stimulating factor precursor - sheep  
N:Alternate names: colony-stimulating factor 2; GM-CSF

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C:Accession: JH0469; S16730

R:McInnes, C.J.; Haig, D.M.

Gene 105, 275-279, 1991

A:Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-st

A:Reference number: JH0469; MUID:92039044; PMID:1937025

A:Accession: JH0469

A:Molecule type: mRNA

A:Residues: 1-144 <MCI>

A:Cross-references: UNIPROT:P28773; UNIPARC:UPI0000128522; GB:X53561; NID:G1800; PIDN:CA

C:Comment: This protein is a glycoprotein cytokine produced and secreted by various cell

C:Superfamily: granulocyte-macrophage colony-stimulating factor

C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell  
 F;1-17/Domain: signal sequence #status predicted <SIG>  
 F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA  
 F;44/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.9%; Score 637; DB 2; Length 144;  
 Best Local Similarity 83.3%; Pred. No. 9,4e-54;  
 Matches 120; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLVVYVSMPTPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60  
 Db 1 MWLQNLGLLVVCSFSAPTQPSVTPRWQHVDAIKEALSLLNDSDTAAVMDTEV 60

Qy 61 SETPDABELTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120  
 Db 61 SEMFDQSEPTCLQRLKLYKQGLRSLTSLTGLTMMASHYKHCPTQETSCETQIITF 120

Qy 121 KSFKNLKDPLFEIPDFDCWKPAOK 144  
 Db 121 KSFKNLKDPLFEIPDFDCWEPVQK 144

RESULT 3  
 FBOGUM  
 granulocyte-macrophage colony-stimulating factor precursor [validated] - human  
 N;Alternate names: colony-stimulating factor 2; GM-CSF  
 C;Species: Homo sapiens (man)  
 C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text\_change 09-Jul-2004  
 C;Accession: C24636; I59065; A2169; A01853; A44175; JCI1090  
 R;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.  
 EMBO J. 4, 2561-2568, 1985

A;Title: Structure of the chromosomal gene for granulocyte-macrophage colony stimulating  
 A;Reference number: A91015; MUID:86030234; PMID:3876930  
 A;Accession: C24636  
 A;Molecule type: DNA  
 A;Residues: 1-144 <MIV>  
 A;Cross-references: UNIPARC:UPI00000358DB; EMBL:X03021; NID:g18158; PIDN  
 R;Kaushansky, K.; O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hagen, F.S.; Adamson, J.W.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 3101-3105, 1986

A;Title: Genomic cloning, characterization, and multilineage growth-promoting activity o  
 A;Reference number: I59065; MUID:86205844; PMID:3486413  
 A;Accession: I59065  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-144 <RES>  
 A;Cross-references: UNIPARC:UPI00000358DB; GB:M13207; NID:g181147; PIDN:AAA98768.1; PID:  
 R;Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6250-6254, 1985

A;Title: Cloning, sequence, and expression of a human granulocyte/macrophage colony-stim  
 A;Reference number: A25169; MUID:85298329; PMID:3898082  
 A;Accession: A25169  
 A;Molecule type: mRNA  
 A;Residues: 1-144 <CAN>  
 A;Cross-references: UNIPARC:UPI00000358DB; GB:M11734; NID:g181149; PIDN:AAA52122.1; PID:  
 R;Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.; Luh, J.; Arai, K.; Rennick,  
 Proc. Natl. Acad. Sci. U.S.A. 82, 4360-4364, 1985

A;Title: Isolation of cDNA for a human granulocyte-macrophage colony-stimulating factor  
 A;Reference number: A01853; MUID:85242684; PMID:3925454  
 A;Accession: A01853  
 A;Molecule type: mRNA  
 A;Residues: 1-144 <LES>  
 A;Cross-references: UNIPARC:UPI00000358DB; GB:M11220; NID:g183363; PIDN:AAA52578.1; PID:  
 R;Wong, G.G.; Mitek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary, A.C.; Luxenberg, D.P.; Jo  
 A.; Clark, S.C.  
 Science 228, 810-815, 1985

A;Title: Human GM-CSF: molecular cloning of the complementary DNA and purification of th  
 A;Reference number: A44175; MUID:85218749; PMID:3923623  
 A;Accession: A44175  
 A;Molecule type: mRNA  
 A;Residues: 1-116, T\*, 118-144 <NON>  
 A;Cross-references: UNIPARC:UPI0000142467; GB:M10663; NID:g181145; PIDN:AAA52121.1; PID:  
 A;Note: parts of this sequence, including the amino end of the mature protein, were conf  
 R;Wen, D.Y.; Huang, B.R.; Cai, L.W.; Si, J.Y.

Acta Biochim. Biophys. Sin. 25, 651-655, 1993  
 A;Title: Amplification of human granulocyte-macrophage colony-stimulating factor cDNA wit  
 A;Reference number: JCI1090  
 A;Accession: JCI1090  
 A;Molecule type: protein  
 A;Residues: 18-21, 'C', 23-96, 'L', 98-144 <WEN>  
 A;Cross-references: UNIPARC:UPI000017368E  
 C;Genetics: GDB:CSF2  
 A;Gene: GDB:CSF2  
 A;Cross-references: GDB:119812; OMIM:138960  
 A;Map position: 5q23.2-5q31.1  
 A;Introns: 53/3; 67/3; 109/3  
 C;Function:  
 A;Description: stimulates the differentiation and proliferation of hematopoietic progeni  
 C;Superfamily: granulocyte-macrophage colony-stimulating factor  
 C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell  
 F;1-17/Domain: signal sequence #status predicted <SIG>  
 F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status experimental  
 F;44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 77.2%; Score 586; DB 1; Length 144;  
 Best Local Similarity 76.4%; Pred. No. 7.1e-49;  
 Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLVVYVSMPTPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60  
 Db 1 MWLQNLGLLVVACISAPARSPSPSTQPSWHEVNAIQEARLLNLSRDTAAEMNETVEV 60

Qy 61 SETPDABELTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120  
 Db 61 SEMFDLQSEPTCLQRLKLYKQGLRSLTKLGLPTMMASHYKQHCPTPETSCATQIITF 120

Qy 121 KSFKNLKDPLFEIPDFDCWKPAOK 144  
 Db 121 ESFKNLKDPLLVIPDFDCWEPVQE 144

RESULT 4  
 FBOGUM  
 granulocyte-macrophage colony-stimulating factor precursor - bovine  
 N;Alternate names: colony-stimulating factor 2; GM-CSF  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
 C;Accession: JI0037  
 R;Maliszewski, C.R.; Schoenborn, M.A.; Cerretti, D.P.; Wignall, J.M.; Picha, K.S.; Cosmar  
 Mol. Immunol. 25, 843-850, 1988

A;Title: Bovine GM-CSF: molecular cloning and biological activity of the recombinant prot  
 A;Reference number: JI0037; MUID:89096971; PMID:3062386  
 A;Accession: JI0037  
 A;Molecule type: mRNA  
 A;Residues: 1-143 <MAL>  
 A;Cross-references: UNIPROT:P11052; UNIPARC:UPI000012851C  
 C;Comment: This glycoprotein induces granulocyte, macrophage, and eosinophil colony forma  
 C;Superfamily: granulocyte-macrophage colony-stimulating factor  
 C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell  
 F;1-17/Domain: signal sequence #status predicted <SIG>  
 F;18-143/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA  
 F;44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.7%; Score 574.5; DB 1; Length 143;  
 Best Local Similarity 75.7%; Pred. No. 8.9e-48;  
 Matches 109; Conservative 16; Mismatches 18; Indels 1; Gaps 1;

Qy 1 MWLQNLGLLVVYVSMPTPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60  
 Db 1 MWLQNLGLLVVCSFSAPTPTATPTRWQHVDAIKEALSLLNHSDDTDVAMNDT-EV 59

Qy 61 SETPDABELTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120  
 Db 60 SEKFDQSEPTCLQRLKLYKQGLQSLTSLMGLTMMATHYKHCPTPETSCGTQFISF 119

Qy 121 KSFKNLKDPLFEIPDFDCWKPAOK 144  
 Db 121 KSFKNLKDPLFEIPDFDCWKPAOK 144







Matches 40; Conservative 27; Mismatches 45; Indels 49; Gaps 9;

Qy 1 MWLQNLLLG-----TVVYSPAPTRQPSVPTRPQHVDIAKEALSLLNN---SSD----- 48  
Db 226 IWMWFLGGENWHNYHAFPSDYRNGA----KWLHLDVHKWIIFLMSKIGLASELERTT 281

Qy 49 ---TAAATMNETVEVSSTFABELTCLQTR-----LKL-----YKQGLRGSL 87  
Db 282 KVIQAOKQOETLNLSEK-QKQKLTLMQTIDHLLNLCIKLEBLEESSITIKEQFKKS F 340

Qy 88 IKLEGPLTMASHYKQHCPTLETSCATOMITFKSFKNLK 128  
Db 341 VEIQESLNLAE-----QVSAATO-ITEKSEKLUK 370

RESULT 12  
G90465  
acyl-CoA dehydrogenase (acd-6) [imported] - Sulfolobus solfataricus  
C/Species: Sulfolobus solfataricus  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C/Accession: G90465  
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Koza, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, E.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A/Description: Sulfolobus solfataricus complete genome.  
A/Reference number: A99139  
A/Accession: G90465  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-400 <KUR>  
A/Cross-references: UNIPROT:Q9TUWG; UNIPARC:UI00000648A2; GB:AEO06641; NID:g13816236; F  
C/Genetics:  
A/Gene: acd-6  
C/Superfamily: acyl-CoA dehydrogenase

Query Match 10.3%; Score 78.5; DB 2; Length 400;  
Best Local Similarity 22.9%; Pred.No.9.2;  
Matches 32; Conservative 23; Mismatches 56; Indels 29; Gaps 3;

Qy 14 YSPAPTRQSP-----VTRPQHVDIAKEALSLLNNSDTAAIMNETVEVSE 62  
Db 175 YVTARTSPPEPNARWKGISMFIVEREWKGKVLNRIETMGLRASNTAEIADFEDVEVPAE 234

Qy 63 TFDAAE-----LTCLOTRLKLYKQLGRSLIKLEGPLTMASHYKQHCPTLETSCA 114  
Db 235 NLIGEENGFKYAMAFDRTRFVGVAQGCVGAALLRMVYTSTQRFAPQSP----- 286

Qy 115 TQMITFKSFKKNLKDFEI 134  
Db 287 --LIGFMVQEKTAEASLTEV 304

RESULT 13  
S70294  
FUN21 protein - yeast (Saccharomyces cerevisiae)  
N/Alternate names: protein VAL031c  
C/Species: Saccharomyces cerevisiae  
C/Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
C/Accession: S70294; S51989; S53563  
R/Vo, D.  
submitted to the EMBL Data Library, April 1996  
A/Reference number: S70291  
A/Accession: S70294  
A/Molecule type: DNA  
A/Residues: 1-760 <VOD>  
A/Cross-references: UNIPROT:P39732; UNIPARC:UPI000013A02E; EMBL:U12980; NID:g1326053; P  
R/Bussay, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; Ouel  
submitted to the EMBL Data Library, August 1994  
A/Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.  
A/Reference number: S51956  
A/Accession: S51989  
A/Molecule type: DNA

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A;Cross-references: UNIPARC:UIP00001792F9; AMLBL:U12980; MIPS:YAL031c  
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A;Note: This sequence has been revised in reference S70291  
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A;Gene: SGD:FUN21  
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A;Map position: 1L  
C;Superfamily: Saccharomyces cerevisiae FUN21 protein  
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F;194-210/Domain: transmembrane #status predicted <TM2>  
F;287-303/Domain: transmembrane #status predicted <TM3>

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707 LROEGFTFRKSLRDGL 723

RESULT 14  
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C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004  
C;Accession: E84429  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; A.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.A.; Vanaken, S.E.; Umayam, L.; Tallon, L.C.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617157  
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A>Status: preliminary  
A:Molecule type: DNA  
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A;Map position: 2  
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RESULT 15  
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C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
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R;Theologas, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A96556  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-490 <STO>  
A:Cross-references: UNIPROT:Q9C8H9; UNIPARC:UPI00000A4D88; GB:AE005173; NID:g11094755; F  
C:Genetics:  
A:Gene: F19C24.8  
A:Map position: 1  
C:Superfamily: Ubiquitin carboxyl-terminal hydrolase

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Db 191 WTQ---LTYLTSQSLKAPTSS-----EGADAVKALFGVNLQSRIRKLGVLNDVTDSTV 239  
QY 52 I-----MNETVEVVSETFDAELTC-----LQTRLKLYKQGLRGLSLIKLEGPLTWM 97  
Db 240 ISKCTLHCQESGESESESVYSLKCHISHEVNHLEGL---KHGLKGELEKTSFALGRT 296  
QY 98 ASHYKQHCPTLETSCATQMITF 120  
Db 297 ALYVKESLIDSLPRYLTVQFVRF 319

Search completed: May 25, 2006, 15:01:36  
Job time : 41 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:01:52 ; Search time 599 Seconds  
(without alignments)  
367.081 Million cell updates/sec

Title: US-10-614-481-9

Perfect score: 759

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	759	100.0	144	25	US-09-587-964-8	Sequence 8, Appl
2	759	100.0	144	25	US-09-587-964A-8	Sequence 8, Appl
3	759	100.0	144	36	US-10-614-481-9	Sequence 9, Appl
4	759	100.0	146	43	US-11-301-800-10	Sequence 10, Appl
5	641	84.5	144	27	US-09-791-537-98077	Sequence 98077, A
6	637	83.9	144	27	US-09-791-537-55369	Sequence 55369, A
7	633	83.4	144	27	US-09-791-537-69622	Sequence 69622, A
8	633	83.4	144	43	US-11-301-800-15	Sequence 15, Appl
9	597	78.7	144	27	US-09-791-537-82598	Sequence 82598, A
10	587	77.3	144	27	US-09-791-537-101680	Sequence 101680, A
11	587	77.3	144	43	US-11-301-800-12	Sequence 12, Appl
12	586	77.2	144	1	PCT-US00-00667-114	Sequence 114, Appl
13	586	77.2	144	1	PCT-US02-31263-18	Sequence 18, Appl
14	586	77.2	144	1	PCT-US02-34502-10	Sequence 10, Appl
15	586	77.2	144	1	PCT-US02-40891-447	Sequence 447, Appl
16	586	77.2	144	1	PCT-US02-40891-448	Sequence 448, Appl
17	586	77.2	144	1	PCT-US02-40891-540	Sequence 540, Appl
18	586	77.2	144	1	PCT-US02-40891-541	Sequence 541, Appl
19	586	77.2	144	1	PCT-US03-12946-2460	Sequence 2460, Appl
20	586	77.2	144	1	PCT-US03-17808-10	Sequence 10, Appl
21	586	77.2	144	1	PCT-US03-29176-3	Sequence 3, Appl
22	586	77.2	144	1	PCT-US03-29176-5	Sequence 5, Appl
23	586	77.2	144	1	PCT-US03-31974-18	Sequence 18, Appl
24	586	77.2	144	1	PCT-US03-32827-83	Sequence 83, Appl
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26	586	77.2	144	1	PCT-US04-30849-14	Sequence 14, Appl
27	586	77.2	144	1	PCT-US04-31524-163	Sequence 163, Appl
28	586	77.2	144	1	PCT-US05-00518-24	Sequence 24, Appl
29	586	77.2	144	11	US-08-105-215-7	Sequence 7, Appl
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32	586	77.2	144	25	US-09-580-474A-17	Sequence 17, Appl
33	586	77.2	144	27	US-09-726-295-15	Sequence 15, Appl
34	586	77.2	144	27	US-09-791-537-55367	Sequence 55367, A
35	586	77.2	144	31	US-10-116-275-217	Sequence 217, Appl
36	586	77.2	144	31	US-10-131-985-15	Sequence 15, Appl
37	586	77.2	144	31	US-10-170-205E-39311	Sequence 39311, A
38	586	77.2	144	32	US-10-287-994-18	Sequence 18, Appl
39	586	77.2	144	33	US-10-331-755-27	Sequence 27, Appl
40	586	77.2	144	34	US-10-410-897-18	Sequence 18, Appl
41	586	77.2	144	34	US-10-410-913-18	Sequence 18, Appl
42	586	77.2	144	34	US-10-410-930-18	Sequence 18, Appl
43	586	77.2	144	34	US-10-410-945-18	Sequence 18, Appl
44	586	77.2	144	34	US-10-410-962-18	Sequence 18, Appl
45	586	77.2	144	34	US-10-410-980-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-587-964-8  
; Sequence 8, Application US/09587964  
; GENERAL INFORMATION:

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; APPLICANT: Fischer, et al.
; TITLE OF INVENTION: IMPROVED DNA VACCINES FOR PETS
; FILE REFERENCE: 454313-2530.1
; CURRENT APPLICATION NUMBER: US/09/587,964
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 60/144,490
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Equus sp.
US-09-587-964-8

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; Sequence 8, Application US/09587964A
; GENERAL INFORMATION:
; APPLICANT: Fischer, et al.
; TITLE OF INVENTION: IMPROVED DNA VACCINES FOR PETS
; FILE REFERENCE: 454313-2530.1
; CURRENT APPLICATION NUMBER: US/09/587,964A
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 60/144,490
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Equus sp.
US-09-587-964A-8

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RESULT 3
US-10-614-481-9
; Sequence 9, Application US/10614481
; GENERAL INFORMATION:
; APPLICANT: Bublot, et al.
; TITLE OF INVENTION: Equine GM-CSF
; FILE REFERENCE: 454313-2334.1
; CURRENT APPLICATION NUMBER: US/10/614,481
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/589,460
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/138,843
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 9
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US-10-614-481-9

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RESULT 4
US-11-301-800-10
; Sequence 10, Application US/11301800
; GENERAL INFORMATION:
; APPLICANT: BUELOW, ROLAND
; APPLICANT: PLATZER, JOSEF
; TITLE OF INVENTION: IMPROVED DNA IMMUNIZATION WITH
; FILE REFERENCE: RECOMBINASE/TRANSPORASE
; FILE REFERENCE: 39691-0013
; CURRENT APPLICATION NUMBER: US/11/301,800
; CURRENT FILING DATE: 2005-12-12
; PRIOR APPLICATION NUMBER: US 60/636,361
; PRIOR FILING DATE: 2004-12-14
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; TYPE: PRT
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US-11-301-800-10

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DB 121 KSFKKNLKDFLFEIPFDCWKPAQK 144

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US-09-791-537-98077
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## RESULT 7

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RESULT 9
US-09-791-82598
; Sequence 82598, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82598
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-791-537-82598

Query Match      78.7%; Score 597; DB 27; Length 144;
Best Local Similarity 77.1%; Pred. No. 1.1e-58;
Matches 111; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLNNSSDTAAIMNETVEVV 60
DB 1 MWLQNLILLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLNNSSDTAAIMNETVDIV 60
QY 61 SETFDAEELTCLOTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
DB 61 CEMFDPQPTCVQTRNLNLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
QY 121 KSFKKNLXDFLFEIPDFDCWKPAQK 144
DB 121 KSFKDSLKNKFLFTIPDFDCWEPK 144

RESULT 10
US-09-791-537-101680
; Sequence 101680, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101680
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-791-537-101680

Query Match      77.3%; Score 587; DB 27; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.5e-57;
Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 MWLQNLILLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLNNSSDTAAIMNETVEVV 60
DB 1 MWLQNLILLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLNNSSDTAAIMNETVDIV 60
QY 61 SETFDAEELTCLOTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
DB 61 CEMFDPQPTCVQTRNLNLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
QY 121 KSFKKNLXDFLFEIPDFDCWKPAQK 144
DB 121 KSFKDSLKNKFLFTIPDFDCWEPK 144

RESULT 11
US-11-301-800-12
; Sequence 12, Application US/11301800
; GENERAL INFORMATION:
; APPLICANT: BUELOW, ROLAND
; APPLICANT: PLATZER, JOSEF
; TITLE OF INVENTION: IMPROVED DNA IMMUNIZATION WITH
; TITLE OF INVENTION: RECOMBINASE/TRANSPPOSASE
; FILE REFERENCE: 39691-0013
; CURRENT APPLICATION NUMBER: US/11/301,800
; CURRENT FILING DATE: 2005-12-12
; PRIOR APPLICATION NUMBER: US 60/636,361
; PRIOR FILING DATE: 2004-12-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-301-800-12

Query Match      77.3%; Score 587; DB 43; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.5e-57;
Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 MWLQNLILLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLNNSSDTAAIMNETVEVV 60
DB 1 MWLQNLILLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLNNSSDTAAIMNETVDIV 60
QY 61 SETFDAEELTCLOTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
DB 61 CEMFDPQPTCVQTRNLNLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
QY 121 KSFKKNLXDFLFEIPDFDCWKPAQK 144
DB 121 KSFKDSLKNKFLFTIPDFDCWGPVK 144

RESULT 12
PCT-US00-06067-114
; Sequence 114, Application PC/TUS0006067
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16PC
; CURRENT APPLICATION NUMBER: PCT/US00/06067
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 09/264,908
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 09/265,992
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-06067-114

Query Match      77.2%; Score 586; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.9e-57;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLNNSSDTAAIMNETVEVV 60
DB 1 MWLQNLILLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLNNSSDTAAIMNETVDIV 60
QY 61 SETFDAEELTCLOTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
DB 61 CEMFDPQPTCVQTRNLNLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
QY 121 KSFKKNLXDFLFEIPDFDCWKPAQK 144
DB 121 KSFKDSLKNKFLFTIPDFDCWGPVK 144
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Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144  
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

## RESULT 13

PCT-US02-32263-18  
; Sequence 18, Application PC/TUS0232263  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Bowe, Carlyn  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
; FILE REFERENCE: 040853-01-5050WO  
; CURRENT APPLICATION NUMBER: PCT/US02/32263  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/334,233  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 60/334,301  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 18  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-32263-18

Query Match 77.2%; Score 586; DB 1; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.9e-57;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
QY 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
Db 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144  
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 14  
PCT-US02-34502-10  
; Sequence 10, Application PC/TUS0234502  
; GENERAL INFORMATION:  
; APPLICANT: Zymogenetics, Inc.  
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS  
; FILE REFERENCE: 01-37PC  
; CURRENT APPLICATION NUMBER: PCT/US02/34502

Query Match 77.2%; Score 586; DB 1; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.9e-57;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
QY 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
Db 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144  
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 15  
PCT-US02-40891-447  
; Sequence 447, Application PC/TUS0240891  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF564PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/40891  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 60/341,811  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/360,000  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/378,950  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/398,008  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: 60/411,355  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/414,984  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/417,611  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/420,246  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: 60/423,623  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/351,360  
; PRIOR FILING DATE: 2002-01-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2222  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 447  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-40891-447

Query Match 77.2%; Score 586; DB 1; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.9e-57;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
QY 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
Db 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144  
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 60/337,586  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-34502-10

Query Match 77.2%; Score 586; DB 1; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.9e-57;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
QY 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
Db 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120  
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144  
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

## RESULT 15

PCT-US02-40891-447  
; Sequence 447, Application PC/TUS0240891  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF564PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/40891  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 60/341,811  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/360,000  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/378,950  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/398,008  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: 60/411,355  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/414,984  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/417,611  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/420,246  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: 60/423,623  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/351,360  
; PRIOR FILING DATE: 2002-01-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2222  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 447  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-40891-447

Query Match 77.2%; Score 586; DB 1; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.9e-57;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
QY 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60  
Db 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAATMNETVEV 60









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; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 540
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-374-540

Query Match      77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.2e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYMPAPTRQPSVTRPWQHVDAIKALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQNLILGTVVYMPAPTRQPSVTRPWQHVDAIKALSLLNNSDTAAIMNETVEV 60
QY 61 SETFDAELTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQPTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120
QY 121 KSFKNLKDFLFPIPPDCWKPAQK 144
Db 121 ESFKENLKDFLFPIPPDCWEPVQE 144

RESULT 8
US-11-429-374-541
; Sequence 541, Application US/11429374
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,374
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 541
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-374-541

Query Match      77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.2e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYMPAPTRQPSVTRPWQHVDAIKALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQNLILGTVVYMPAPTRQPSVTRPWQHVDAIKALSLLNNSDTAAIMNETVEV 60
QY 61 SETFDAELTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQPTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120
QY 121 KSFKNLKDFLFPIPPDCWKPAQK 144
Db 121 ESFKENLKDFLFPIPPDCWEPVQE 144
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; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 541
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-374-541

Query Match      77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.2e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYMPAPTRQPSVTRPWQHVDAIKALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQNLILGTVVYMPAPTRQPSVTRPWQHVDAIKALSLLNNSDTAAIMNETVEV 60
QY 61 SETFDAELTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQPTCLQRLKLYKQGLRSLIKLEGLPTMASHYKQHCPTLETSCATQMITF 120
QY 121 KSFKNLKDFLFPIPPDCWKPAQK 144
Db 121 ESFKENLKDFLFPIPPDCWEPVQE 144

RESULT 9
US-11-429-276-447
; Sequence 447, Application US/11429276
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 447
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-447

Query Match      77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.2e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYMPAPTRQPSVTRPWQHVDAIKALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQNLILGTVVYMPAPTRQPSVTRPWQHVDAIKALSLLNNSDTAAIMNETVEV 60
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; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 541
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-541

Query Match          77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.1e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLGTVVYVSMAPTRQSPVTRPQWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
Db 1 MWLQNLGTVVACISAPARSPSTQWHEVNAIQEARLLNLSRDTAAEMNETVEVI 60

Qy 61 SHTPDABELTCLQRLKLYKQGLRSLIKLEGPLTMMASHYKQHCPTLETSCATQITF 120
Db 61 SHMFDLQEPCTCLQRLKLYKQGLRSLIKLEGPLTMMASHYKQHCPTLETSCATQITF 120

Qy 121 KSFKENLKDGLFELPFDCWKPAQK 144
Db 121 ESFKENLKDGLLVIPFDCWEPVQE 144

RESULT 13
US-11-429-373-324
; Sequence 324, Application US/11429373
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,373
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 324
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-374-324

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Best Local Similarity 76.4%; Pred. No. 1.1e-57;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

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Qy 121 KSFKENLKDGLFELPFDCWKPAQK 144
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; Sequence 324, Application US/11429374
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,374
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
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; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-374-324

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RESULT 15
US-11-429-276-324
; Sequence 324, Application US/11429276
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
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; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
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; NUMBER OF SEQ ID NOS: 2222
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; ORGANISM: Homo sapiens
US-11-429-276-324

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**BEST AVAILABLE COPY**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 00:41:25 ; Search time 3045 Seconds  
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Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_pat.\*

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5: gb\_pr.\*

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10: gb\_vl.\*

11: gb\_ov.\*

12: gb\_hcg.\*

13: gb\_in.\*

14: gb\_on.\*

15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	435	100.0	435	2 AX057390	AX057390 Sequence
3	435	100.0	435	2 AX067832	AX067832 Sequence
4	432	99.3	438	14 AF448481	AF448481 Equus cab
5	419.8	96.5	779	14 AY040203	AY040203 Equus cab
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18	332.6	76.5	444	2 AR254522	AR254522 Sequence

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ALIGNMENTS

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DEFINITION Sequence 8 from patent US 6645740.  
ACCESSION AR429724  
VERSION AR429724.1 GI:40190061  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 435)  
AUTHORS Bublot,M., Perez,J.M. and Andreoni,C.M.P.  
TITLE Nucleic acids encodings equine GM-CSF  
JOURNAL Patent: US 6645740-A 8 11-NOV-2003;  
Merical Limited and Merical LLC; London;  
GBX;

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DB 421 CCAGCCCAAGAGTAA 435

RESULT 2
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LOCUS AX057390 435 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 8 from Patent WO077210.
ACCESSION AX057390
VERSION AX057390.1 GI:12310131
KEYWORDS
SOURCE Equus sp.
ORGANISM Equus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
1
REFERENCE
AUTHORS Bublot,M., Perez,J.M. and Andreoni,C.M.
TITLE Equine granulocyte-macrophage colony-stimulating factor (gm-csf)
JOURNAL Patent: WO 0077210-A 8 21-DEC-2000;
MERRIAL (FR)
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RESULT 4
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LOCUS AF448481 438 bp mRNA linear MAM 12-AUG-2002
DEFINITION Equus caballus granulocyte-macrophage colony-stimulating factor
(GM-CSF) mRNA, partial cds.
ACCESSION AF448481
VERSION AF448481.2 GI:22208937
KEYWORDS
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LOCUS AX067832 435 bp DNA linear PAT 19-JAN-2001
DEFINITION Sequence 69 from Patent WO077043.
ACCESSION AX067832
VERSION AX067832.1 GI:12329710
KEYWORDS
SOURCE Equus sp.
ORGANISM Equus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
1
REFERENCE
AUTHORS Fischer,L.J., barzu-le Roux,S. and Audonnet,J.C.
TITLE Dna vaccines for pets and sport animals
JOURNAL Patent: WO 0077043-A 69 21-DEC-2000;
MERRIAL (FR)
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RESULT 4
AF448481
LOCUS AF448481 438 bp mRNA linear MAM 12-AUG-2002
DEFINITION Equus caballus granulocyte-macrophage colony-stimulating factor
(GM-CSF) mRNA, partial cds.
ACCESSION AF448481
VERSION AF448481.2 GI:22208937
KEYWORDS
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SOURCE      Equus caballus (horse)
ORGANISM    Equus caballus
REFERENCE   1 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
TITLE       1 (bases 1 to 438)
JOURNAL     Vecchione,A., D'Mello,F., Kanellos,T.S., Howard,C.R., Hamblin,A.S.
AUTHORS     Vecchione,A., D'Mello,F., Kanellos,T.S., Howard,C.R., Hamblin,A.S.
TITLE       2 (bases 1 to 438)
JOURNAL     Direct Submission
AUTHORS     Submitted (16-NOV-2001) Department of Pathology and Infectious
TITLE       Diseases, Royal Veterinary College, Royal College Street, London
JOURNAL     NW1 0TU, UK
REFERENCE   3 (bases 1 to 438)
AUTHORS     Vecchione,A., D'Mello,F., Kanellos,T.S., Howard,C.R., Hamblin,A.S.
TITLE       Direct Submission
JOURNAL     Submitted (12-AUG-2002) Department of Pathology and Infectious
TITLE       Diseases, Royal Veterinary College, Royal College Street, London
JOURNAL     NW1 0TU, UK
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QY 421 CCAGCCCAAG 432
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DEFINITION Equus caballus granulocyte-macrophage colony-stimulating-factor
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ACCESSION AY040203
VERSION    AY040203.2 GI:16740524
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ORGANISM   Equus caballus
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AUTHORS     Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
JOURNAL     Mauel,S., Commandeur,U. and Steinbach,F.
REFERENCE  2 (bases 1 to 779)
AUTHORS     Mauel,S., Commandeur,U. and Steinbach,F.
TITLE       Direct Submission
JOURNAL     Submitted (14-JUN-2001) Virology, Free University Berlin,
REFERENCE  3 (bases 1 to 779)
AUTHORS     Koenigin-Luise-Str.49, Berlin 14 195, Germany
TITLE       Direct Submission
JOURNAL     Mauel,S., Commandeur,U. and Steinbach,F.
REMARK      Sequence update by submitter
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Best Local Similarity 99.3%; Pred. No. 1.1e-100;
Matches 432; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
DB 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATCCATCAAGAGGCCCTG 120

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Db      61  CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Qy      121  AGCCTTCTGAACAACAGTAGTGACACTGCTCTATCATGAATGAAACAGTAGTAGAGTCGTC 180
Db      121  AGCCTTCTGAACAACAGTAGTGACACTGCTCTATCATGAATGAAACAGTAGTAGAGTCGTC 180
Qy      181  TCTGAAAGCTTTGAGCGCGAGGAGTGACATGCCCTGCGAGCTCGCCTGAAGCTGTACAAA 240
Db      181  TCTGAAAGCTTTGAGCGCGAGGAGTGACATGCCCTGCGAGCTCGCCTGAAGCTGTACAAA 240
Qy      241  CAGGCTTGGCGGGCAGGCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCAGCCAC 300
Db      241  CAGGCTTGGCGGGCAGGCTCATCAAGCTCGAAGGCCCTTTAAACCATGATGCCAGCCAC 300
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Db      301  TACAAGCAGCATGCCCCCCCCCCTGGAATCTCTGTGTGCAACCCAGATGATCACTTC 360
Qy      361  AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGATGCCGTTTGAAGCTGTGGAAG 420
Db      361  AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGATGCCGTTTGAAGCTGTGGAAG 420
Qy      421  CCAGCCCAAGATA 435
Db      420  CCAGCCCAAGATA 434

RESULT 6
OOGMCSF      Ovine GM-CSF mRNA for granulocyte-macrophage colony stimulating
LOCUS      factor.
DEFINITION      X55991
ACCESSION      X55991
VERSION      1
KEYWORDS      cytokine; granulocyte-macrophage colony stimulating factor.
SOURCE      Ovis aries (sheep)
ORGANISM      Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.

REFERENCE      1
AUTHORS      O'Brien, P.M., Rothel, J.S., Seow, H.F. and Wood, P.R.
TITLE      Cloning and sequencing of the cDNA for ovine granulocyte-macrophage
JOURNAL      colony-stimulating factor (GM-CSF)
PUBMED      Immunol. Cell Biol. 69 (pt 1), 51-55 (1991)
1869289
REFERENCE      2
AUTHORS      O'Brien, P.
TITLE      Direct Submission
JOURNAL      Submitted (12-OCT-1990) O'Brien P., Commonwealth Scientific &
Industrial Research, (CSIRO) Division of Animal Health, Private Bag
No 1, Parkville Vic 3052, Australia
COMMENT      Stimulates bone marrow progenitor cells to proliferate and
differentiate.
FEATURES      Location/Qualifiers
source      1..432
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ORIGIN      factor"
Query Match      83.5%; Score 363.2; DB 14; Length 432;
Best Local Similarity 90.0%; Pred. No. 1.2e-85;
Matches 389; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy      1  ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGACCCACCC 60
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Qy      61  CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db      61  CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Qy      121  AGCCTTCTGAACAACAGTAGTGACACTGCTCTATCATGAATGAAACAGTAGTAGAGTCGTC 180
Db      121  AGCCTTCTGAACAACAGTAGTGACACTGCTCTATCATGAATGAAACAGTAGTAGAGTCGTC 180
Qy      181  TCTGAAAGCTTTGAGCGCGAGGAGTGACATGCCCTGCGAGCTCGCCTGAAGCTGTACAAA 240
Db      181  TCTGAAAGCTTTGAGCGCGAGGAGTGACATGCCCTGCGAGCTCGCCTGAAGCTGTACAA 240
Qy      241  CAGGCTTGGCGGGCAGGCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCAGCCAC 300
Db      241  CAGGCTTGGCGGGCAGGCTCATCAAGCTCTCAGGGCTCTTGACCATGATGCCAGCCAC 300
Qy      301  TACAAGCAGCATGCCCCCCCCCCTGGAATCTCTGTGTGCAACCCAGATGATCACTTC 360
Db      301  TACAAGAAACACTGCCCCCCCCCAGGAACTCTCTGTGAAACCCAGATATATCACTTC 360
Qy      361  AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGAAGCTGTGGAAG 420
Db      361  AAAAGTTTCAAAAAGAACTGAAGATTTCTTTTATCATCTCCCTTTGACTGCTGGGAA 420
Qy      421  CCAGCCCAAGAA 432
Db      421  CCAGCCCAAGAA 432

RESULT 7
OOGMCSF      Capra hircus granulocyte-macrophage colony stimulating factor
LOCUS      (GM-CSF) mRNA, complete cds.
DEFINITION      DQ010419
ACCESSION      DQ010419
VERSION      DQ010419.1
KEYWORDS      GI:62825817
SOURCE      Capra hircus (goat)
ORGANISM      Capra hircus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Capra.
REFERENCE      1
AUTHORS      Shu, D.O., Cao, S.X., Mao, D.G., Wu, Z.M. and Yang, L.G.
TITLE      Cloning and Sequence Analysis of Capra Hircus
JOURNAL      Granulocyte-macrophage Colony Stimulating Factor (GM-CSF)
REFERENCE      2
AUTHORS      Shu, D.O., Cao, S.X., Mao, D.G., Wu, Z.M. and Yang, L.G.
TITLE      Direct Submission
JOURNAL      Submitted (18-APR-2005) The Animal Breed Institute, Nanjing
Agricultural University, Nanjing, Jiangsu 210095, China
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source
gene
CDS

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ORIGIN

Query Match 83.4%; Score 363; DB 14; Length 435;  
Best Local Similarity 89.7%; Pred. No. 1.3e-85;  
Matches 390; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
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DB 181 TCTGAAAGCTTTGACGCGAGGAGCTGACATGCCGTCGAGACTCGCTGAAGCTGTACAAA 240  
QY 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
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QY 301 TACAAGCAGACTGCCCCCCCCACCTCGGAAACTTCTGTGCAACCCAGATGATCACTTC 360  
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QY 361 AAAAGTTTCAAAAGAACTGAAGATTTCTGTTTGAGATCCCTTTGACTGCTGGAG 420  
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QY 421 CCAGCCCAAGAGTAA 435  
DB 421 CCAGTCCAGAGTAA 435

RESULT 8

OOGMCSFR 495 bp mRNA linear MAM 18-APR-2005  
LOCUS Ovine mRNA for granulocyte-macrophage stimulating factor (GM-CSF).  
DEFINITION X53561  
ACCESSION X53561.1 GI:1800  
VERSION granulocyte-macrophage colony stimulating factor; signal peptide.  
KEYWORDS Ovis aries (sheep)  
SOURCE Ovis aries  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Caprinae; Ovis.

REFERENCE

1  
McInnes, C.J. and Haig, D.M.  
Cloning and expression of a cDNA encoding ovine  
granulocyte-macrophage colony-stimulating factor  
Gene 105 (2), 275-279 (1991)  
JOURNAL PUBMED 1937025  
REFERENCE 2 (bases 1 to 495)  
AUTHORS McInnes, C.J.  
TITLE Direct Submission  
Submitted (20-JUN-1990) McInnes C.J., Moredun Research Institute,  
408 Gilmerton Rd., Edinburgh EH17 7JH, Scotland, UK  
JOURNAL Location/Qualifiers  
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ORIGIN

Query Match 83.4%; Score 363; DB 14; Length 495;  
Best Local Similarity 89.7%; Pred. No. 1.4e-85;  
Matches 390; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
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DB 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
QY 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
DB 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
QY 181 TCTGAAAGCTTTGACGCGAGGAGCTGACATGCCGTCGAGACTCGCTGAAGCTGTACAAA 240  
DB 181 TCTGAAAGCTTTGACGCGAGGAGCTGACATGCCGTCGAGACTCGCTGAAGCTGTACAAA 240  
QY 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
DB 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
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DB 301 TACAAGAAATACCTGCCCCCCCCACCCAGGAACTTCTGTGAAACCCAGATTATCACTTC 360  
QY 361 AAAAGTTTCAAAAGAACTGAAGATTTCTGTTTGAGATCCCTTTGACTGCTGGAG 420  
DB 361 AAAAGTTTCAAAAGAACTGAAGATTTCTGTTTGAGATCCCTTTGACTGCTGGAG 420  
QY 421 CCAGCCCAAGAGTAA 435  
DB 421 CCAGTCCAGAGTAA 448

RESULT 9

OOGMCSFR 432 bp mRNA linear MAM 14-SEP-1994  
LOCUS Cervus elaphus granulocyte-macrophage colony-stimulating factor  
DEFINITION U14392  
ACCESSION U14392  
VERSION U14392.1 GI:537895  
KEYWORDS Cervus elaphus (red deer)  
SOURCE Cervus elaphus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Cervidae; Cervinae; Cervus.  
REFERENCE 1 (bases 1 to 432)  
AUTHORS Lockhart, E.A.

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Cloning and sequencing of cervine GM-CSF		D21074	Unpublished		D21074.1	GI:497829			
	2 (bases 1 to 432)			Lockhart, E.A.			Sus scrofa (pig)			
	Direct Submission			Submitted (05-SEP-1994)			Sus scrofa			
	Research Laboratory, University of Otago, Union St., Dunedin, New Zealand						Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.			
FEATURES source	Location/Qualifiers		1	Inumaru, S. and Takamatsu, H.		1	Inumaru, S. and Takamatsu, H.			
	1. .432			cDNA cloning of porcine granulocyte-macrophage colony-stimulating factor			cDNA cloning of porcine granulocyte-macrophage colony-stimulating factor			
	/organism="Cervus elaphus"			Immunol. Cell Biol. 73 (5), 474-476 (1995)			Immunol. Cell Biol. 73 (5), 474-476 (1995)			
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gene	1. .432		Inumaru, S.	Direct Submission		Submitted (06-OCT-1993)	Shigeki Inumaru, National Institute of Animal Health, Biological Products Research Division; 3-1-1, Kannondai, Tsukuba, Ibaraki 305, Japan (Tel:81-298-38-8624, Fax:81-298-38-7880)			
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	Best Local Similarity			82.4%; Score 358.4; DB 14; Length 432;			82.4%; Score 358.4; DB 14; Length 432;			
	Matches 386; Conservative			0; Mismatches 46; Indels 0; Gaps 0;			0; Mismatches 46; Indels 0; Gaps 0;			
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Db	1		61	CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG		61	CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG			
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	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
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	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
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	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
QY	1		61	CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG		61	CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG			
	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
Db	1		61	CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG		61	CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG			
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	1			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC			
QY	1		61	CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG		61	CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG			
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Qy 421 CCAGCCCAAGAGTAA 435

Db 421 CCAGCCCAAGAGTGA 435

RESULT 11

AX067831

LOCUS AX067831

DEFINITION Sequence 68 from Patent WO0077043.

ACCESSION AX067831

VERSION AX067831.1 GI:12329709

KEYWORDS

SOURCE Felis.catus (cat)

ORGANISM Felis catus

REFERENCE

AUTHORS Fischer,L.J., barzu-le Roux,S. and Audonnet,J.C.

TITLE Dna vaccines for pets and sport animals

JOURNAL Patent: WO 0077043-A 68 21-DEC-2000;

FEATURES

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Location/Qualifiers

/organism="Felis catus"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9885"

ORIGIN

Query Match 76.5%; Score 332.6; DB 2; Length 435;

Best Local Similarity 85.3%; Pred. No. 1.6e-77;

Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 1 ATGTGGCTGCAGAACCTGCTTTCTTGGGCACTGTGGTTA CAGATGCCGCCACCCACC 60

Db 1 ATGTGGCTGCAGAACCTGCTTTCTTGGGCACTGTGGTTA CAGATGCCGCCACCCACC 60

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Db 121 AGCCTTCTGAACAAACAGTAGTGAAATACTGTGTGATGAATGAACAGTAGAAGTCGTC 180

Qy 181 TCTGAAACGTTTGAACCGGAGAGTGACATGCCCTGCAGACTCGGCTGAAGCTGTACAAA 240

Db 181 TCTGAAATGTTTGAACCTGAGGAGCGGAAATGCCTGCAGACTCACTAAAGCTGTACGAG 240

Qy 241 CAGGCTTCGGGGCAGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300

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Qy 301 TACAAGCAGACTGCGCCGCCACCTCGAAACTTCTGTGCAACCGACATGATCACCTTC 360

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Qy 421 CCAGCCCAAGAGTAA 435

Db 421 CCAGTCAAGAGTGA 435

RESULT 12

SSU67175

LOCUS SSU67175

DEFINITION Sus scrofa granulocyte macrophage-colony stimulating factor

(GM-CSF) mRNA, complete cds.

ACCESSION U67175

VERSION U67175.1 GI:1513327

KEYWORDS

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE

1 (bases 1 to 435)

AUTHORS Gloster,S.E., Sandeman,R.M. and Strom,A.D.G.

TITLE Cloning of a cDNA and gene encoding porcine granulocyte macrophage-colony stimulating factor (GM-CSF)

JOURNAL Unpublished

AUTHORS Gloster,S.E., Sandeman,R.M. and Strom,A.D.G.

TITLE Direct Submision

JOURNAL Submitted (19-AUG-1996) Animal Health, CSIRO, Park Drive, Melbourne, VIC 3052, Australia

FEATURES

source

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Location/Qualifiers

/organism="Sus scrofa"

/mol\_type="mRNA"

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primer\_bind

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/note="based on the porcine genomic DNA sequence"

ORIGIN

Query Match 76.5%; Score 332.6; DB 14; Length 435;

Best Local Similarity 85.3%; Pred. No. 1.6e-77;

Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Db 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTCTGCAGCATCTCCGCTCCACC 60

Qy 61 CGCCAAACCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120

Db 61 CGCCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120

Qy 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180

Db 121 AGCCTTCTTAACAACAGTAATGACACAGGGCTGTGATGAATGAACCGTAGACGTCGTC 180

Qy 181 TCTGAAACGTTTGAACCGGAGAGTGACATGCCCTGCAGACTCGGCTGAAGCTGTACAAA 240

Db 181 TGTGAAATGTTTGAACCCCGAGGCGGACATCGCTGCAGACTCGGCTGAACCTGTACAA 240

Qy 241 CAGGCTTCGGGGCAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300

Db 241 CAGGCTTCGGGGCAGGCTCATCAAGCTCGAAGGCCCTTGACCTGTGTGCCCAGCAC 300

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Db 301 TATGAGCAGACTGCGCCCTCTACCGAGGAAACTTCTGTGAAACCGACGTATACCTTC 360

Qy 361 AAAAGTTTCAAAAGAACTGAAGGATTTTCTGTGTTGAGATCCCTTTGACTGCTGGGAG 420

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Qy      421 CCAGCCCAAGAGTAA 435
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Db      421 CCAGTCAAAAAGTAA 435

RESULT 13
LOCUS   BD211587
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
ACCESSION BD211587
VERSION   BD211587.1 GI:33021357
KEYWORDS  JP 2002516104-A/93.
SOURCE    Felis catus (cat)
ORGANISM  Felis catus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
          Felinae; Felis.
REFERENCE 1 (bases 1 to 444)
AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE      Canine and feline immunoregulatory proteins, nucleic acid molecules
          and method of using the same.
JOURNAL    Patent: JP 2002516104-A 93 04-JUN-2002;
          HESKA CORP
COMMENT    OS Felis catus (cat)
          PN JP 2002516104-A/93
          PD 04-JUN-2002
          PF 28-MAY-1999 JP 2000551002
          PR 29-MAY-1998 US 60/087306
          PT GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
          C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
          PC A61K39/395,
          PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
          PC C07K14/54,
          PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
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          PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
          and feline immunoregulatory proteins, nucleic acid CC
          molecules and
          CC method of using the same
          FH Key Location/Qualifiers
          FT CDS (10)..(441).

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Query Match 76.5%; Score 332.6; DB 2; Length 444;
Best Local Similarity 85.3%; Pred. No. 1.6e-77;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy      1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCCGCACCCACC 60
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Db      430 CCAGACCAGAGTAA 444

RESULT 14
LOCUS   BD211588/c
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
          and method of using the same.
ACCESSION BD211588
VERSION   BD211588.1 GI:33021358
KEYWORDS  JP 2002516104-A/94.
SOURCE    Felis catus (cat)
ORGANISM  Felis catus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
          Felinae; Felis.
REFERENCE 1 (bases 1 to 444)
AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE      Canine and feline immunoregulatory proteins, nucleic acid molecules
          and method of using the same
          Patent: JP 2002516104-A 94 04-JUN-2002;
          HESKA CORP
COMMENT    OS Felis catus (cat)
          PN JP 2002516104-A/94
          PD 04-JUN-2002
          PF 28-MAY-1999 JP 2000551002
          PR 29-MAY-1998 US 60/087306
          PT GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
          C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
          PC A61K39/395,
          PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
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          G01N33/15,
          PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
          and feline immunoregulatory proteins, nucleic acid CC
          molecules and
          CC method of using the same
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Query Match 76.5%; Score 332.6; DB 2; Length 444;
Best Local Similarity 85.3%; Pred. No. 1.6e-77;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy      1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCCGCACCCACC 60
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Db      435 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCCGCACCCACC 376

Qy      61 CGCCAAACCCAGCCCTGTCACCTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 120
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Db 315 AGCCCTTCTGAACAAACAGTAGTGAATTAACCTGCTGTGATGAATGAAGCAGTAGAAGTCGTC 256  
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Qy 241 CAGGGCTTCGCGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
Db 195 CAGGGCTTCAGCGGAGCCTCATCAGCCTCAAGAGCCTCTGAGAATGATGCCAACCAT 136  
Qy 301 TACAAGCAGACTGCCGCCCAACCTCGGAACTTCTGTGCAACCCAGATGATACCTTC 360  
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Db 15 CCAGACCAGATAA 1

RESULT 15  
LOCUS AR241565 444 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 119 from patent US 6471957.  
ACCESSION AR241565  
VERSION AR241565.1 GI:27287274  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 444)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 Immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 119 29-OCT-2002;  
Heska Corporation; Fort Collins, CO;  
EPX;

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Query Match 76.5%; Score 332.6; DB 2; Length 444;  
Best Local Similarity 85.3%; Pred.No.1.6e-77;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
Qy 1 ATGTGGCTGCAGAACTGCTTCTTCTGGSCACTGTGGTTTACAGCATGCCGCAACCCACC 60  
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Qy 61 CGCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGGAGGCCCTG 120  
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Job time : 3047 secs

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 00:33:29 ; Search time 449 Seconds  
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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	435	100.0	435	4	Aaf28953 Equine gr
3	363.2	83.5	432	2	Aaq24294 Ovine GM-
4	332.6	76.5	435	4	ABZ80827 Feline gr
5	332.6	76.5	444	3	Aaz55575 Feline GM
6	332.6	76.5	444	3	Aaz55576 Feline GM
7	332.6	76.5	798	2	Aaq64864 CHEP-2 ge
8	331.6	76.2	435	12	ADQ76022 Human GM-
9	331.6	76.2	435	15	Aef81846 Human GM-
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11	331	76.1	435	2	Aav83189 Granulocy
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13	331	76.1	435	4	ABZ80826 Feline gr
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25	331	76.1	781	14	ADY16394 DNA encod
26	331	76.1	781	14	ADZ26536 Human GMS
27	331	76.1	781	14	ABZ54678 DNA encod
28	331	76.1	787	1	Aan50364 Human gra
29	331	76.1	787	2	Aaq84865 Clone pcd
30	331	76.1	789	3	AAA35017 Human ade
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32	331	76.1	789	4	AAH28217 Nucleotid
33	331	76.1	789	10	ABZ96833 Human nuc
34	331	76.1	789	11	ABD20682 Human pul
35	331	76.1	900	14	ADZ08738 Adenovira
36	331	76.1	900	14	ABE95949 Oncolytic
37	331	76.1	900	15	AAE75748 Recombina
38	331	76.1	1172	14	ADZ08733 Adenovira
39	331	76.1	1172	14	ABE95944 Oncolytic
40	331	76.1	1172	15	AAE75743 Recombina
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## ALIGNMENTS

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ID ABZ80828 standard; DNA; 435 BP.

XX AC ABZ80828;

XX DT 27-JUN-2003 (first entry)

XX DE Equine granulocyte-macrophage colony stimulating factor gene.

XX KW Granulocyte-macrophage colony stimulating factor; GM-CSF; ds; gene;

XX KW antibacterial; antiviral; vaccine; animal; immunogen; DMRIE;

XX KW cationic lipid; quaternary ammonium salt; canine distemper virus;

XX KW canine parainfluenza virus; canine herpes virus; feline herpes virus;

XX KW equine herpes virus; dog; cat; horse.

XX OS Equus caballus.

XX FH Key Location/Qualifiers

XX FT CDS 1..435

XX FT /\*tag= a

XX FT /product= "Equine GM-CSF"

XX PN WO200077043-A2.

XX PD 21-DEC-2000.

XX PF 08-JUN-2000; 2000WO-FR001592.

XX PR 10-JUN-1999; 99FR-00007604.

XX PR 19-JUL-1999; 99US-0144490P.

XX XX (MERI-) MERIAL.

XX PA Fischer LJ, Barzu-Le Roux S, Audomnet JF;

XX PI WPI; 2001-071259/08.

XX DR P-PSDB; ABP98711.

XX DR DNA vaccine containing plasmid and cationic lipid containing quaternary

XX PT ammonium salt, useful for protecting pets and sports animals against,

PT e.g. herpes virus.  
XX  
PS Example 10; Fig 26; 109pp; French.  
XX  
CC The invention relates to a novel DNA vaccine against pathogens that  
CC affect pets and sports animals comprises a plasmid containing a sequence,  
CC expressible in vivo, that encodes an immunogen from the relevant pathogen  
CC and a cationic lipid containing a quaternary ammonium salt, particularly  
CC N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium  
CC (DMRIE). The immunogens are particularly taken from canine distemper  
CC virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes  
CC virus (CHV), feline herpes virus type 1 (FHV-1), equine herpes virus type  
CC 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of  
CC a immunogenic stimulation factor especially a granulocyte-macrophage  
CC colony stimulation factor (GM-CSF) to enhance the immunogenic response.  
CC The vaccines, which may be multivalent, are particularly used to protect  
CC dogs, cats and horses against bacterial and viral diseases, particularly  
CC those caused by the Paramyxoviridae. Formulations with the quaternary  
CC ammonium salt provide a better immune response and thus more efficient  
CC protection, particularly when administered subcutaneously. This sequence  
CC represents the gene encoding an equine GM-CSF used in the invention  
XX  
SQ Sequence 435 BP; 109 A; 132 C; 105 G; 89 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 435; DB 4; Length 435;  
Best Local Similarity 100.0%; Pred. No. 1.4e-111;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGTTTACAGCATGCCCGCACCCACC 60  
Db 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGTTTACAGCATGCCCGCACCCACC 60  
  
QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTTG 120  
Db 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTTG 120  
  
QY 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180  
Db 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180  
  
QY 181 TCTGAAACGTTTGACGCGAGGAGCTGACATCGCTGCAGACTCGCTGAAGCTGTACAAA 240  
Db 181 TCTGAAACGTTTGACGCGAGGAGCTGACATCGCTGCAGACTCGCTGAAGCTGTACAAA 240  
  
QY 241 CAGGCGTTTCGGGGCAGCTCATCAAGCTCGAAGCCCTTGAACATGATGCCAGCCAC 300  
Db 241 CAGGCGTTTCGGGGCAGCTCATCAAGCTCGAAGCCCTTGAACATGATGCCAGCCAC 300  
  
QY 301 TACAAGCAGCACTGCCCGCCACCTCGGAACTTCTGTGCAACCCAGATGATCACCTTC 360  
Db 301 TACAAGCAGCACTGCCCGCCACCTCGGAACTTCTGTGCAACCCAGATGATCACCTTC 360  
  
QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGAGATCCCGTTTGACTGTGGAAG 420  
Db 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGAGATCCCGTTTGACTGTGGAAG 420  
  
QY 421 CCAGCCCAAGAGTAA 435  
Db 421 CCAGCCCAAGAGTAA 435  
  
RESULT 2  
ID AAF28953  
XX AAF28953 standard; DNA; 435 BP.  
XX  
AC AAF28953;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Equine granulocyte-macrophage colony stimulating factor gene.  
XX  
KW Immunostimulatory; granulocyte-macrophage colony stimulating factor;  
KW horse; reverse transcriptase PCR; colony formation; blood; cytotoxicity;

KW inflammation; vector; adjuvant; immunogen; vaccination; vaccine;  
KW equine herpes; tetanus; Borrelia burgdorferi; rabies; gene; ds.  
OS Equus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..435  
FT /\*tag= a  
FT /product= "equine GM-CSF"  
XX  
PN WO200077210-A1.  
XX  
PD 21-DEC-2000.  
XX  
PF 08-JUN-2000; 2000WO-FR001590.  
XX  
PR 10-JUN-1999; 99US-0138843P.  
XX  
PA (MERI-) MERIAL.  
XX  
PI Bublot M, Perez JM, Andreoni CMP;  
XX  
DR WPI; 2001-080689/09.  
DR P-PSDB; AAB37147.  
XX  
PT Novel DNA encoding equine granulocyte-macrophage colony-stimulating  
PT factor, useful as adjuvant for vaccines and as non-specific  
PT immunostimulant.  
XX  
PS Claim 3; Fig 1; 34pp; French.  
XX  
CC This sequence represents the gene encoding a horse granulocyte-macrophage  
CC colony stimulating factor (GM-CSF). The gene was isolated from horse  
CC lymphocytes using a reverse transcriptase PCR method with primers  
CC AAF28954-AAF28960. GM-CSF induces colony formation in various types of  
CC blood cells and particularly induces cytotoxicity of macrophages;  
CC stimulates antibody-dependent cytotoxicity, and causes recruitment of  
CC leucocytes to sites of inflammation. Vectors containing the gene or the  
CC protein itself, are useful as adjuvants in immunogenic or vaccinating  
CC compositions for horses, e.g. for protection against equine herpes,  
CC tetanus, Borrelia burgdorferi, rabies etc. Also as non-specific  
CC stimulators of the immune system. In a specific example, plasmid pJP097,  
CC containing the sequence for equine GM-CSF was used to transform CHO-K1  
CC cells and the transformants grown for 48 hours. The culture supernatant  
CC was then added to culture medium being used to grow porcine bone marrow  
CC cells. After 14 days, the mean number of colonies per culture box was 12-  
CC 15, compared with none for cells grown in absence of GM-CSF. Equine GM-  
CC CSF allows a reduction in the amount of immunogenic/vaccinating component  
CC required, and may induce a response in animals that would otherwise be  
CC non-responders  
XX  
SQ Sequence 435 BP; 109 A; 132 C; 105 G; 89 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 435; DB 4; Length 435;  
Best Local Similarity 100.0%; Pred. No. 1.4e-111;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGTTTACAGCATGCCCGCACCCACC 60  
Db 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGTTTACAGCATGCCCGCACCCACC 60  
  
QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTTG 120  
Db 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTTG 120  
  
QY 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180  
Db 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180  
  
QY 181 TCTGAAACGTTTGACGCGAGGAGCTGACATCGCTGCAGACTCGCTGAAGCTGTACAAA 240  
Db 181 TCTGAAACGTTTGACGCGAGGAGCTGACATCGCTGCAGACTCGCTGAAGCTGTACAAA 240

QY 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAGCCAC 300  
 DB |||||  
 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAGCCAC 300  
 QY 301 TACAGCAGCACTGCCCCCACCCTTGGAACTTCTGTGCAACCCAGATGATCACTTTC 360  
 DB |||||  
 301 TACAGCAGCACTGCCCCCACCCTTGGAACTTCTGTGCAACCCAGATGATCACTTTC 360  
 QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGTAGATCCCGTTTGACTGCTGGAAG 420  
 DB |||||  
 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGTAGATCCCGTTTGACTGCTGGAAG 420  
 QY 421 CCAGCCCAAGTAA 435  
 DB |||||  
 421 CCAGCCCAAGTAA 435

RESULT 3  
 ID AAQ24294 standard; DNA; 432 BP.  
 AC AAQ24294;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-OCT-1992 (first entry)  
 XX  
 DE Ovine GM-CSF gene.  
 XX  
 KW Granulocyte-macrophage colony-stimulating factor; immuno-depression;  
 KW vaccine adjuvants; cytokine; ss.  
 OS  
 XX Ovis aries.  
 FH Key  
 FT CDS  
 FT 1..432  
 /tag= c  
 /note= "ovine GM-CSF"  
 FT sig\_peptide  
 FT 1..51  
 /tag= a  
 /note= "putative signal sequence"  
 FT misc\_feature  
 FT 1..25  
 /tag= d  
 /note= "GM-N PCR primer"  
 FT mat\_peptide  
 FT 52..432  
 /tag= b  
 /note= "mature protein"  
 FT misc\_feature  
 FT 408..432  
 /tag= e  
 /note= "GM-C PCR primer"

PN W09205255-A.  
 XX  
 PD 02-APR-1992.  
 XX  
 PF 13-SEP-1990; 90AU-00002294.  
 XX  
 PR 13-SEP-1990; 90AU-00002294.  
 PR 21-MAR-1991; 91AU-00005175.  
 XX  
 PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX  
 PI Wood PR, Rothe JS, Seow HF;  
 XX  
 DR WPI: 1992-150483/18.  
 DR P-PSDB; AAR23662.  
 XX  
 PT DNA encoding ovine cytokine(s) - used to prepare recombinant cytokine(s)  
 PT for treatment of immuno-depression in sheep.  
 XX  
 PS Claim 2; Fig 3; 79pp; English.  
 XX  
 CC The sequence is that of the ovine granulocyte-macrophage colony  
 CC stimulating factor (GM-CSF) gene which can be used in the prodn. of

CC recombinant gamma-interferon, a cytokine-like molecule. The ovine  
 CC cytokines will be useful in the intensive livestock industries such as  
 CC live animal export trade, feed-lots and intensive rearing industries,  
 CC where animals are subjected to great environmental challenge with  
 CC infectious diseases, partic. respiratory infections, and are more prone  
 CC to immunodepressive effects. The cytokines may be used for treatment or  
 CC prophylaxis to maintain, stimulate or enhance immunoresponsiveness. They  
 CC may also be useful as natural adjuvants for vaccines for sheep and  
 CC cattle. See also AAQ24293-305, AAQ2311-15, AAQ24317-18 and AAQ25857-58.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX

SQ Sequence 432 BP; 101 A; 138 C; 103 G; 90 T; 0 U; 0 Other;

Query Match 83.5%; Score 363.2; DB 2; Length 432;

Best Local Similarity 90.0%; Pred. No. 1.8e-91;

Matches 389; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCATCTGGTTTACAGCATGCCGACCCACC 60  
 DB |||||  
 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCATCTGGTTTACAGCATGCCGACCCACC 60  
 QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
 DB |||||  
 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
 QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAAACAGTAGAAGTCGTC 180  
 DB |||||  
 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAAACAGTAGAAGTCGTC 180  
 QY 181 TCTGAAAGCTTTGACGCGGAGGAGCTGACATGCCCTGCAGACTCGCCTGAAGCTGTACAA 240  
 DB |||||  
 181 TCTGAAAGCTTTGACTCCAGGAGCCGACATGCCCTGCAGACTCGCCTGAGCTGTACAA 240  
 QY 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAGCCAC 300  
 DB |||||  
 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAGCCAC 300  
 QY 301 TACAAAGCAGCACTGCCCCCACCCTTGGAACTTCTGTGCAACCCAGATGATCACTTTC 360  
 DB |||||  
 301 TACAAAGCAGCACTGCCCCCACCCTTGGAACTTCTGTGCAACCCAGATGATCACTTTC 360  
 QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGTAGATCCCGTTTGACTGCTGGAAG 420  
 DB |||||  
 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGTAGATCCCGTTTGACTGCTGGAAG 420  
 QY 421 CCAGCCCAAGTAA 432  
 DB |||||  
 421 CCAGCCCAAGTAA 432

# RESULT 4

ABZ80827  
 ID ABZ80827 standard; DNA; 435 BP.  
 XX  
 AC ABZ80827;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 27-JUN-2003 (first entry)  
 XX  
 DE Feline granulocyte-macrophage colony stimulating factor gene 3R4.  
 XX  
 KW Granulocyte-macrophage colony stimulating factor; GM-CSF; ds; gene;  
 KW antibacterial; antiviral; vaccine; animal; immunogen; DMRIE;  
 KW cationic lipid; quaternary ammonium salt; canine distemper virus;  
 KW canine parainfluenza virus; canine herpes virus; feline herpes virus;  
 KW equine herpes virus; dog; cat; horse.  
 XX  
 OS Felis catus.  
 XX  
 FH Key  
 FT CDS  
 FT 1..435  
 /tag= a  
 /product= "feline GM-CSF 3R4"

```

XX WO200077043-A2.
XX
XX
XX PD 21-DEC-2000.
XX PF 08-JUN-2000; 2000WO-FR001592.
XX PR 10-JUN-1999; 99FR-00007604.
XX PR 19-JUL-1999; 99US-0144490P.
XX PA (MERI-) MERIAL.
XX
XX PI Fischer LJ, Barzu-Le Roux S, Audonnet JF;
XX DR WPI; 2001-071259/08.
XX DR P-PSDB; AHP98710.
XX
XX DNA vaccine containing plasmid and cationic lipid containing quaternary
XX ammonium salt; useful for protecting pets and sports animals against,
XX e.g. herpes virus.
XX
XX Example 9; Fig 24; 109pp; French.
XX
XX The invention relates to a novel DNA vaccine against pathogens that
XX affect pets and sports animals comprises a plasmid containing a sequence,
XX expressible in vivo, that encodes an immunogen from the relevant pathogen
XX and a cationic lipid containing a quaternary ammonium salt, particularly
XX N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium
XX (DMRIE). The immunogens are particularly taken from canine distemper
XX virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes
XX virus (CHV), feline herpes virus type 1 (FHV-1), equine herpes virus
XX type 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of
XX an immunogenic stimulation factor especially a granulocyte-macrophage
XX colony stimulation factor (GM-CSF) to enhance the immunogenic response.
XX The vaccines, which may be multivalent, are particularly used to protect
XX dogs, cats and horses against bacterial and viral diseases, particularly
XX those caused by the Paramyxoviridae. Formulations with the quaternary
XX ammonium salt provide a better immune response and thus more efficient
XX protection, particularly when administered subcutaneously. This sequence
XX represents the gene encoding a feline GM-CSF used in the invention.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 435 BP; 116 A; 121 C; 102 G; 96 T; 0 U; 0 Other;

Query Match 76.5%; Score 332.6; DB 4; Length 435;
Best Local Similarity 85.3%; Pred. No. 7e-83;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
DB 1 ATGTGGCTGCAGAACCTGCTTCTTGGGCACTGTGGTTTACAGCATCTGCACCCACC 60
QY 61 CGCCCAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
DB 61 AGTTCAACCCAGCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCTCTG 120
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
DB 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
QY 181 TCTGAACGTTTGGCCGAGGAGCTGACATCCCTGCAGACTCGCTGAAGCTGTACAAA 240
DB 181 TCTGAACGTTTGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 241 CAGGGCTTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 CAGGGCTTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
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DB 301 TACAAGAGCACTGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 360
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGTAGATCCCGCTTTGACTGCTGGAAG 420

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DB 361 AAAAATTTCAAGAGAACTCTGAAGGATTTTCTGTTTAAACATCCCTTTGACTGCTGGAAG 420
QY 421 CCAGCCCAAGAGTAA 435
DB 421 CCAGTCAAGAGTGA 435

RESULT 5
ID AAZ55575 standard; cDNA; 444 BP.
XX AAZ55575;
XX AC AAZ55575;
XX DT 14-MAR-2000 (first entry)
XX DE Feline GMCSF cDNA.
XX KW Granulocyte macrophage colony-stimulating factor; GMCSF; antibody;
XX KW feline; inhibitor; immune response; immunoregulation; tumour; cancer;
XX KW autoimmune disease; vaccine; ss.
XX OS Felis catus.
XX FH Key Location/Qualifiers
XX CDS 10..444
XX FT /*tag= a
XX FT /product= "Feline GMCSF"
XX PN WO9961618-A2.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US011942.
XX PR 29-MAY-1998; 98US-0087306P.
XX (HESK-) HESKA CORP.
XX PA
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX DR WPI; 2000-072623/06.
XX DR P-PSDB; AAY58229.
XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX PT useful for treating or preventing e.g. tumors or autoimmune disease.
XX PS Claim 1k; Page 251-252; 264pp; English.
XX
XX Sequences AAZ55575-255580 represent cDNA sequences encoding feline
XX granulocyte macrophage colony-stimulating factor (GMCSF). The invention
XX relates to canine interleukin-4 (IL-4), canine or feline Flt-3 ligand,
XX canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5,
XX canine IL-13, feline interferon-alpha (IFN-alpha) and feline GMCSF, and
XX nucleotides which encode these immunoregulatory proteins. The proteins,
XX their associated nucleic acids, specific antibodies and inhibitors may be
XX used as vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans). They
XX may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase the
XX response from a co-administered antigen. The nucleotide sequences can
XX also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for modulators
XX of activity, while the antibodies may be used in detection, and in drug
XX targeting
XX
XX Sequence 444 BP; 119 A; 127 C; 104 G; 94 T; 0 U; 0 Other;

Query Match 76.5%; Score 332.6; DB 3; Length 444;
Best Local Similarity 85.3%; Pred. No. 7e-83;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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QY 1 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCCGCACCCACC 60  
 |||||  
 Db 10 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATCTCTGCACCCACC 69  
 |||||  
 QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCGCCTG 120  
 |||||  
 Db 70 AGTTCAACCCAGCTCTGTCTACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGGCGCCTG 129  
 |||||  
 QY 121 AGCCTTCTCAACAAACAGTAGTACACTGCTGTCTATCATGAATGAACAGTAGAAGTCGTC 180  
 |||||  
 Db 130 AGCCTTCTGAACAAACAGTAGTGAATACTGTGTGATGAAGACGATGAAGTCGTC 189  
 |||||  
 QY 181 TCTGAAACGTTTACGCCGAGGAGCTGACATGCTTGCAGACTCGCCTGAAGCTGTACAAA 240  
 |||||  
 Db 190 TCTGAAATGTTGACCTCGAGGCGGAATGCTTGCAGACTCACCTAAAGCTGTACGAG 249  
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 QY 241 CAGGCTTCGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
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 Db 250 CAGGCTTCAGGGGAGCCTCATCAAGCTCAAGGAGCCTCTGAGAATGATGCCAACCAT 309  
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 QY 301 TACAAGCAGACTGCCCGCCCGCCCTGGAACTTCTGTGCAACCCAGATGATCACTTC 360  
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 Db 310 TACAAGCAGACTGCCCGCCCTTACTCGGAACGCCCTGTGAACCCAGACTATCACCTTC 369  
 |||||  
 QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTTCTGTTTGAATCCCGTTTGACTGCTGGAAG 420  
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 Db 370 AAAAATTTCAAAAGAGAATCTGAAGGATTTTCTGTTTAAACAACCCCTTTGACTGCTGGGA 429  
 |||||  
 QY 421 CCAGCCCAAGTA 435  
 |||||  
 Db 430 CCAGACCAGAGTAA 444  
 |||||

## RESULT 6

AAZ55576/c  
 ID AAZ55576 standard; cDNA; 444 BP.  
 XX  
 AC AAZ55576;  
 XX  
 DT 14-MAR-2000 (first entry)  
 XX  
 DE Peline GMCSF cDNA complement.  
 XX  
 KW Granulocyte macrophage colony-stimulating factor; GMCSF; antibody;  
 KW feline; inhibitor; immune response; immunoregulation; tumour; cancer;  
 KW autoimmune disease; vaccine; ss.  
 XX  
 OS Felis catus.  
 FH  
 FT Key Location/Qualifiers  
 CDS complement(1..435)  
 FT /\*tag= a  
 FT /product= "Peline GMCSF"

XX WO9961618-A2.  
 PN  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99WO-US011942.  
 XX  
 PR 29-MAY-1998; 98US-0087306P.  
 XX  
 PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX  
 DR WPI; 2000-072623/06.  
 XX  
 DR P-PSDB; AAY58229.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX

PS Claim 1k; Page 253; 264pp; English.

XX Sequences AAZ55575-255580 represent cDNA sequences encoding feline  
 CC granulocyte macrophage colony-stimulating factor (GMCSF). The invention  
 CC relates to canine interleukin-4 (IL-4), canine or feline flt-3 ligand,  
 CC canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5,  
 CC canine IL-13, feline interferon-alpha (IFN-alpha) and feline GMCSF, and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting  
 XX

SQ Sequence 444 BP; 94 A; 104 C; 127 G; 119 T; 0 U; 0 Other;

Query Match 76.5%; Score 332.6; DB 3; Length 444;

Best Local Similarity 85.3%; Pred. No. 7e-83;

Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCCGCACCCACC 60  
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Db 435 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATCTCTGCACCCACC 376  
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QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCGCCTG 120  
 |||||

Db 375 AGTTCAACCCAGCTCTGTCTACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGGCGCCTG 316  
 |||||

QY 121 AGCCTTCTGAACAAACAGTAGTGAATACTGTGTGATGAAGACGATGAAGTCGTC 180  
 |||||

Db 315 AGCCTTCTGAACAAACAGTAGTGAATACTGTGTGATGAAGACGATGAAGTCGTC 256  
 |||||

QY 181 TCTGAAACGTTTACGCCGAGGAGCTGACATCCCTGCAGACTCGCTGAAGCTGTACAAA 240  
 |||||

Db 255 TCTGAAATGTTTACGCCGAGGAGCGGAATGCCCTGCAGACTCACCTAAAGCTGTACGAG 196  
 |||||

QY 241 CAGGCTTCGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300  
 |||||

Db 195 CAGGCTTCAGGGGAGCCTCATCAAGCTCGAAGGCCCTTGAAGATGATGCCAACCAT 136  
 |||||

QY 301 TACAAGCAGACTGCCCGCCCGCCCTTCTGTGCAACCCAGATGATCACCTTC 360  
 |||||

Db 135 TACAAGCAGACTGCCCGCCCGCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACCTTC 76  
 |||||

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTTCTGTTTGAATCCCGTTTGACTGCTGGAAG 420  
 |||||

Db 75 AAAAATTTCAAAAGAGAATCTGAAGGATTTTCTGTTTAAACAACCCCTTTGACTGCTGGGA 16  
 |||||

QY 421 CCAGCCCAAGTA 435

Db 15 CCAGACCAGAGTAA 1

## RESULT 7

AAQ64864  
 ID AAQ64864 standard; DNA; 798 BP.

XX AAQ64864;

XX AC AAQ64864;

XX DT 25-MAR-2003 (revised)

XX DT 10-MAR-2003 (revised)

XX DT 07-NOV-1994 (first entry)

XX DE CHEP-2 gene.

XX Cytokine; chimerism enhancing factors; porcine; transplant;

KW xenogeneic cells; bone marrow; African swine fever; Hog cholera;  
XX Pseudorabies; ss.  
OS

XX Sus scrofa.

XX Key Location/Qualifiers  
FT sig\_peptide 30..99 /\*tag= a  
FT /note= "signal"  
FT mat\_peptide 100..464 /\*tag= b  
FT

XX WO9409803.A1.

XX 11-MAY-1994.

XX 26-OCT-1993; 93WO-US010295.

XX 27-OCT-1992; 92US-00967188.

XX 08-OCT-1993; 93US-00133979.

XX (BIOT-) BIOTRANSPLANT INC.

XX Ponath PD, Rosa MD, Monroy RL, Schacter BZ, Hawley RJ;  
XX

XX WPI; 1994-167114/20.

XX P-PSDB; AAR54818.

XX Porcine cytokine Chimerism Enhancing Factors (CHEFs) and DNA - used to  
XX enhance xenograft tolerance.

XX Claim 40; Page 72; 113pp; English.

XX The sequence is that of a porcine cytokine gene designated chimerism  
XX enhancing factor (CHEF-2). The cytokine can be used for improving  
XX engraftment, stabilisation and proliferation of tissues, esp. bone marrow  
XX cells, in xenogeneic transplantation. The cytokine may be used to prevent  
XX or treat various swine diseases, e.g. African swine fever, Hog cholera,  
XX Pseudorabies, etc. See also AAQ64863-80. (Updated on 10-MAR-2003 to add  
XX missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)  
XX

XX Sequence 798 BP; 208 A; 215 C; 180 G; 195 T; 0 U; 0 Other;

Query Match 76.5%; Score 332.6; DB 2; Length 798;  
Best Local Similarity 85.3%; Pred. No. 8.8e-83;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGGTTTACAGCATGCCGCCACCCACC 60

DB 30 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGGTTTACAGCATGCCGCCACCCACC 89

QY 61 LQCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 120

DB 90 TCGCCACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 149

QY 121 AGCCTTCTGAACAAACAGTAGTGACATGCTGTATCATGAATGAACAGTAGATCGTC 180

DB 150 AGCCTTCTGAACAAACAGTAGTGACATGCTGTATCATGAATGAACAGTAGATCGTC 209

QY 181 TCTGAAGCTTTGACGCGAGGAGCTGCATCGCTGCAGACTCGCTGAAGCTGTACAAA 240

DB 210 TGTGAAGCTTTGACGCGAGGAGCTGCATCGCTGCAGACTCGCTGAAGCTGTACAAA 269

QY 241 CAGGGCTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300

DB 270 CAGGGCTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 329

QY 301 TACAAGCAGACTGCCCCCCCACCTCTGTGGAACCTTCTGTGGAACCCAGATGATCACCTTC 360

DB 330 TATGAGCAGACTGCCCCCCCACCTCTGTGGAACCTTCTGTGGAACCCAGATGATCACCTTC 389

QY 361 AAAGTTTCAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCGTTTCACTGCTGGAG 420

DB 390 AAAAGTTTCAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGG 449  
QY 421 CCAGCCAGCAAGTAA 435  
DB 450 CCAGTCAAAAAGTAA 464

RESULT 8

ADQ76022 standard; DNA; 435 BP.

XX ADQ76022;

XX 07-OCT-2004 (first entry)

XX Human GM-CSF wild-type coding sequence.

XX ds; gene; human; GM-CSF; codon optimisation; protein production.

XX Homo sapiens.

XX WO2004059556-A2.

XX 15-JUL-2004.

XX 23-DEC-2003; 2003WO-EP014850.

XX 23-DEC-2002; 2002DE-01060805.

XX (GENE-) GENEART GMBH.

XX Raab D, Graf M, Notka F, Wagner R;

XX WPI; 2004-543639/52.

XX Computer optimization of a nucleotide sequence for a protein comprises  
XX evaluating test sequences with a quality function to determine the  
XX optimum sequence.  
XX Disclosure; SEQ ID NO 1; 83pp; German.

XX The present invention relates to a method of optimising a coding sequence  
XX for expression of a protein, based on the amino acid sequence of the  
XX protein. This involves the use of a computer to generate a test sequence  
XX with m optimisation positions determined for a defined region, in which  
XX positions the codon usage is varied. The optimum codon usage at such  
XX positions is determined by means of a power function. The steps are  
XX reiterated with different regions of the sequence, with the optimised  
XX codons previously identified being left unchanged during subsequent  
XX steps. The method can be used for expression of proteins. The present  
XX sequence is the human GM-CSF wild-type coding sequence.

XX Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;

Query Match 76.2%; Score 331.6; DB 12; Length 435;  
Best Local Similarity 85.3%; Pred. No. 1.3e-82;  
Matches 370; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGGTTTACAGCATGCCGCCACCCACC 60

DB 1 ATGTGGCTGCAGAGCTGCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 60

QY 61 CGCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 120

DB 61 CGCTCGCCAGCCCGCAGCAGCGAGCCCTGGGAGCATGGAATGCCATCAGGAGGCCCG 120

QY 121 AGCCTTCTGAACAAACAGTAGTGACATGCTGTATCATGAATGAACAGTAGATCGTC 180

DB 121 CGTCTCTTGAACCTCAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGATC 180

QY 181 TCTGAAAAGCTTTGACGCGAGGAGCTGCATGCCCTGCAGACTCGCTGAAGCTGTACAA 240

DB 181 TCAGAAATGTTTGACCTCCAGGAGCCGACCTGCTGCCTACAGACCCGCTGGAGCTGTA 240

QY 241 CAGGGCTTGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAGCCAC 300  
DB AEF81846 standard; DNA; 435 BP.  
AC AEF81846;  
XX  
XX  
DT 20-APR-2006 (first entry)  
DE Human GM-CSF wild-type (10CpG) DNA.  
XX ds; gene; vector; expression; GM-CSF.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 1..435  
FT /\*tag= a  
FT /product= "GM-CSF"  
XX  
XX WO2006015789-A2.  
XX  
XX 16-FEB-2006.  
XX  
XX 03-AUG-2005; 2005WO-EP008423.  
XX  
XX 03-AUG-2004; 2004DE-10037611.  
XX 03-AUG-2004; 2004DE-10037652.  
XX (GENE-) GENEART GMBH.  
XX  
XX Notka F, Graf M, Leikam D, Wagner R, Raab D;  
XX  
XX WPI; 2006-193389/20.  
XX P-PSDB; AEF81847.  
XX GENBANK; M11220.  
XX  
XX Process to modify nucleic acid for incorporation in a vectored expression  
XX in e.g. transgenic animals, medical therapy or vaccines.  
XX  
XX Example 3; SEQ ID NO 23; 99pp; German.  
XX  
XX This invention describes a novel process for modifying nucleic acid for a  
XX vectored expression modulation by targeted insertion or removal of CpG di-  
XX nucleotides. The invention also describes modified nucleic acids and  
XX vector expressions. The process commences with the expression from tissue  
XX of a sample substance containing the target nucleic acid sequence,  
XX followed by its modification to increase or decrease the genetic  
XX expression of CpG di-nucleotides present, by degeneration of the genetic  
XX code. The modified target nucleic acid sequence is cloned with the  
XX modified number of CpG di-nucleotides in a suitable vector expression,  
XX operationally linked with a suitable transcription regulatory sequence.  
XX The modified target nucleic acid sequence is then expressed in a modified  
XX expression system. The novel process can be used to modify nucleic acids  
XX for incorporation in a vectored expression in e.g. transgenic animals,  
XX medical therapy or vaccines. The process extends the usable range of

CC Genetic expression. This sequence encodes human wild-type GM-CSF  
CC containing 10CpG, used in the process of the invention.  
XX  
SQ Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;  
Query Match 76.2%; Score 331.6; DB 15; Length 435;  
Best Local Similarity 85.3%; Pred. No. 1.3e-82;  
Matches 370; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 1 ATGTGGCTGCAGAACCTCTCTCTCTGGGCACTGTGGTTTACAGATGCCACCCACC 60  
DB 1 ATGTGGCTGCAGAACCTCTCTCTCTGGGCACTGTGGTTTACAGATGCCACCCACC 60  
QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
DB 61 CGCTCGCCAGCCCGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG 120  
QY 121 AGCCTTCTGAACACAGTAGTAGACTGCTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180  
DB 121 CGTCTCTGAAACCTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180  
QY 181 TCTGAACGTTTTCACGCGGAGGAGCTGACATGSCCTGCAGACTCGCTGAACTGTACAAA 240  
DB 181 TCAGAAATGTTTTCACCTCCAGGAGCCGACCTGCTTACAGACCCGCTGGAGCTGTACAG 240  
QY 241 CAGGCTTTCGCGGGCAGGCTCATCAAGCTCGAAGGCCCTTGGACCATGATGCCAGCCAC 300  
DB 241 CAGGCTTTCGCGGGCAGGCTCATCAAGCTCGAAGGCCCTTGGACCATGATGCCAGCCAC 300  
QY 301 TACAAGCAGCAGCTGCCCCCCCCCAGCCCTGGAACCTTCTGTGCAACCCAGATGATCCTTC 360  
DB 301 TACAAGCAGCAGCTGCCCCCCCCCAGCCCTGGAACCTTCTGTGCAACCCAGATGATCCTTC 360  
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTCTGTTTGGATCCCGTTTGACTGCTGGAG 420  
DB 361 GAAAGTTTCAAAAAGAACCTGAAGGATTTCTGTTTGGATCCCGTTTGACTGCTGGAG 420  
QY 421 CCAGCCCAAGAGTA 434  
DB 421 CCAGTCCAGGAGTA 434  
RESULT 10  
AAF55040  
ID AAF55040 standard; DNA; 432 BP.  
XX  
XX AAF55040;  
XX  
XX 15-MAY-2001 (first entry)  
XX  
XX Nucleotide sequence of GM-CSF gene clone 3R4.  
XX  
XX Capsid protein; FCV strain 431; FCV strain G1; vaccine; cat; ds.  
XX  
XX Felis catus.  
XX Key Location/Qualifiers  
FT CDS 1..432  
FT /\*tag= a  
FT /product= "GM-CSF"  
XX  
XX WO200105934-A2.  
XX  
XX 25-JAN-2001.  
XX  
XX 13-JUL-2000; 2000WO-FR002051.  
XX  
XX 16-JUL-1999; 99FR-00009421.  
XX 11-FEB-2000; 2000FR-00001761.  
XX (MERI-) MERIAL.  
XX Audonnet JF, Baudu PGN, Brunet SC;  
PI



QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGTAGATCCCGTTTGACTGCTGGAAG 420  
 |||||  
 Db 361 GAAAGTTTCAAAAGAGAACCTGAAGGACTTTCTGTTGTATCCCTTTGACTGCTGGAG 420  
 |||||  
 QY 421 CCAGGCCAGAGTAA 435  
 |||||  
 Db 421 CCAGTCCAGGAGTGA 435  
 |||||

RESULT 12  
 AAA64392  
 ID AAA64392 standard; DNA; 435 BP.  
 AC AAA64392;  
 XX  
 XX 20-DEC-2000 (first entry)  
 XX  
 DE DNA sequence of granulocyte macrophage colony stimulating factor.  
 XX  
 XX Expression cassette; insect cell; insect secretion competent polypeptide;  
 KW fusion protein; protein production;  
 KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200050616-A2.  
 PN  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 23-FEB-2000; 2000WO-CA000188.  
 XX  
 PR 24-FEB-1999; 99US-00256694.  
 XX  
 PA (UYTE-) UNIV TECHNOLOGIES INT INC.  
 XX  
 XX Iatrou K, Farrell PJ, Behie LA;  
 PI WPI; 2000-524624/47.  
 XX  
 XX Expression cassette contains a promoter, signal peptide, secretion  
 PT competent polypeptide and heterologous protein for production and  
 PT secretion of heterologous peptides from eukaryotic cells.  
 XX  
 PS Example 5; Fig 6; 55pp; English.  
 CC  
 CC The specification describes an expression cassette which is useful for  
 CC the secretion of a heterologous protein from insect cells. The protein is  
 CC expressed as a fusion protein, and is encoded by a polynucleotide  
 CC comprising, in the 5' to 3' direction, a promoter, a signal peptide, an  
 CC insect secretion competent polypeptide which is not an immunoglobulin Fc  
 CC region and a heterologous protein with the coding sequences linked in  
 CC frame. The expression cassette and vector are used for the production of  
 CC heterologous peptides and proteins in insect and mammalian cell. The  
 CC present sequence encodes a human granulocyte macrophage colony  
 CC stimulating factor (GM-CSF) (a secretion component). It is used to  
 CC construct expression cassettes of the invention  
 XX  
 SQ Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;  
 Query Match 76.1%; Score 331; DB 3; Length 435;  
 Beat Local Similarity 85.1%; Pred. No. 2e-82;  
 Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTTCTTGGCAGCTGTGTACAGATGCCCGCCACCCACC 60  
 |||||  
 Db 1 ATGTGGCTGCAGAGCTGTGCTCTTGGCAGCTGTGTACAGATGCCCGCCACCCACC 60  
 |||||  
 QY 61 CGCCCAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGCATCAAGGAGGCCCTG 120  
 |||||  
 Db 61 CGCTGCCAGCCAGCCAGCAGGAGCCCTGGGAGCATGTGAATGCCATCAGAGGCCCGG 120  
 |||||  
 QY 121 AGCCTTCTGAACAACAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
 |||||

Db 121 CQTCTCTGAAACCTGAGTAGACACATGCTGCTGAGATGAATGAACAGTAGAAGTCATC 180  
 QY 181 TCTGAAACCTTTGACGCGGAGGAGCTGACATGCTGCAGACTCGCCTGAAGCTGTACAAA 240  
 |||||  
 Db 181 TCAGAAATGTTTGACCTCCAGGAGCGACCTGCCTACAGACCGCCTGGAGCTGTAAAG 240  
 |||||  
 QY 241 CAGGGCTTTCGGGGGAGGCTTCATCAAGCTTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300  
 |||||  
 Db 241 CAGGGCTTTCGGGGGAGGCTTCATCAAGCTTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300  
 |||||  
 QY 301 TACAAGCAGCACTGCCCGCCACCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360  
 |||||  
 Db 301 TACAAGCAGCACTGCCCGCCACCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360  
 |||||  
 QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGTAGATCCCGTTTGACTGCTGGAAG 420  
 |||||  
 Db 361 GAAAGTTTCAAAAGAGAACCTGAAGGACTTTCTGTTGTATCCCTTTGACTGCTGGAG 420  
 |||||  
 QY 421 CCAGGCCAGAGTAA 435  
 |||||  
 Db 421 CCAGTCCAGGAGTGA 435  
 |||||

RESULT 13  
 ABZ80826  
 ID ABZ80826 standard; DNA; 435 BP.  
 XX  
 AC ABZ80826;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 27-JUN-2003 (first entry)  
 XX  
 DE Feline granulocyte-macrophage colony stimulating factor gene 3R3.  
 XX  
 KW Granulocyte-macrophage colony stimulating factor; GM-CSF; ds; gene;  
 KW antibacterial; antiviral; vaccine; animal; immunogen; DMRIE;  
 KW cationic lipid; quaternary ammonium salt; canine distemper virus;  
 KW canine parainfluenza virus; canine herpes virus; feline herpes virus;  
 KW equine herpes virus; dog; cat; horse.  
 XX  
 OS Felis catus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..435  
 FT /tag= a  
 FT /product= "feline GM-CSF 3R3"  
 XX  
 PN WO200077043-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PD 08-JUN-2000; 2000WO-FR001592.  
 PF  
 XX 10-JUN-1999; 99FR-00007604.  
 PR 19-JUL-1999; 99US-0144490P.  
 XX  
 XX (MERI-) MERIAL.  
 PA  
 XX  
 XX Fischer LJ, Barzu-Le Roux S, Audonnet JF;  
 PI WPI; 2001-071259/08.  
 DR P-PSDB; ABP98709.  
 DR  
 XX DNA vaccine containing plasmid and cationic lipid containing quaternary  
 PT ammonium salt, useful for protecting pets and sports animals against,  
 PT e.g. herpes virus.  
 XX  
 PS Example 9; Fig 22; 109pp; French.  
 CC  
 CC The invention relates to a novel DNA vaccine against pathogens that  
 CC affect pets and sports animals comprises a plasmid containing a sequence,  
 CC expressible in vivo, that encodes an immunogen from the relevant pathogen  
 CC and a cationic lipid containing a quaternary ammonium salt, particularly

CC N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium  
CC (DMRIE). The immunogens are particularly taken from canine distemper  
CC virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes  
CC virus (CHV), feline herpes virus type 1 (FHV-1), equine herpes virus type  
CC 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of  
CC a immunogenic stimulation factor especially a granulocyte-macrophage  
CC colony stimulation factor (GM-CSF) to enhance the immunogenic response.  
CC The vaccines, which may be multivalent, are particularly used to protect  
CC dogs, cats and horses against bacterial and viral diseases, particularly  
CC those caused by the Parvoviridae. Formulations with the quaternary  
CC ammonium salt provide a better immune response and thus more efficient  
CC protection, particularly when administered subcutaneously. This sequence  
CC represents the gene encoding a feline GM-CSF used in the invention.  
CC (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 435 BP; 117 A; 120 C; 101 G; 97 T; 0 U; 0 Other;

Query Match 76.1%; Score 331; DB 4; Length 435;  
Best Local Similarity 85.1%; Pred. No. 2e-82;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCGCCACCCACC 60  
DB 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCGCCACCCACC 60  
QY 61 CGCCAAACCCAGCCCTGCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
DB 61 AGTTCACCCAGCTGTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
QY 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGTATCATGAATGAAACAGTAGAAGTCGTC 180  
DB 121 AGCCTTCTGAAACACAGTAGTGAAATACTGTGTGATGATGAAGCAGTAGAAGTCGTC 180  
QY 181 TCTGAAACGTTTGACCCGAGGAGCTGACATCCCTGCAGACTCGCTGAAGCTGTACAAA 240  
DB 181 TCTGAAATGTTTGACCTTGAGGAGCGAAATGCTTGCAGACTCACCTAAAGCTGTACGAG 240  
QY 241 CAGGCTTCGCGGGCAGCTCATCAAGTCGAAAGCCCTTACCATGATGATGCCAGCCAC 300  
DB 241 CAGGCTTCGCGGGCAGCTCATCAAGTCGAAAGCCCTTACCATGATGATGCCAGCCAC 300  
QY 301 TACAAGCAGCACTGCCCCCACCCTCGGAAACTTCTGTGCAACCCAGATGATCACTTC 360  
DB 301 TACAAGCAGCACTGCCCCCTTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 360  
QY 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420  
DB 361 AAAAATTTCAAAAGAAATCTGAAGATTTCTGTTTAAATCCCTTTGACTGCTGGAAA 420  
QY 421 CCAGCCCAAGTAA 435  
DB 421 CCAGTCAAGAGTGA 435

RESULT 14  
ACCT78877  
ID ACC78877 standard; DNA; 435 BP.  
XX  
AC ACC78877;  
XX  
DT 02-SEP-2003 (first entry)  
XX  
DE Human GM-CSF encoding DNA.  
XX  
KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;  
KW granulocyte-macrophage colony stimulating factor; GM-CSF; human; gene;  
KW ds.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS Location/Qualifiers  
1..435  
/\*tag= a

FT  
XX  
PN W02003031464-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 09-OCT-2002; 2002WO-US032263.  
XX  
PR 10-OCT-2001; 2001US-0328523P.  
PR 19-OCT-2001; 2001US-0344692P.  
PR 28-NOV-2001; 2001US-0334233P.  
PR 07-NOV-2001; 2001US-0334301P.  
PR 07-JUN-2002; 2002US-0387292P.  
PR 25-JUN-2002; 2002US-0391777P.  
PR 17-JUL-2002; 2002US-0396594P.  
PR 16-AUG-2002; 2002US-0404249P.  
PR 28-AUG-2002; 2002US-0407527P.  
XX  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
XX  
PI De Fries S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;  
XX  
DR WPI; 2003-449162/42.  
DR P-PSDB; ABR55847.  
XX  
PT Remodeling a peptide, by removing a saccharyl subunit from the peptide to  
PT form truncated glycan, and adding or deleting glycosyl groups to a  
PT peptide and/or adding modifying group of a peptide to remodel the  
PT peptide.  
XX  
PS Example; Fig 59A; 900pp; English.  
XX  
CC The invention relates to a cell-free, in vitro method of remodeling a  
CC peptide. The method involves removing a saccharyl subunit from the  
CC peptide, thus forming a truncated glycan, and contacting the truncated  
CC glycan with at least one glycosyltransferase and at least one glycosyl  
CC donor under conditions suitable to transfer at least one glycosyl donor  
CC to the truncated glycan, thus remodeling the peptide. Conjugates can be  
CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,  
CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,  
CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin  
CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)  
CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)  
CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)  
CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha  
CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-  
CC glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2  
CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-  
CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,  
CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth  
CC hormone (HGH) peptide, and a modifying group, where the modifying group  
CC is covalently attached to the peptide through an intact glycosyl linking  
CC group. The method is useful for a cell-free, in vitro method of  
CC remodeling the above mentioned peptides. The present sequence represents  
CC a human GM-CSF encoding DNA  
XX  
SQ Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;

Query Match 76.1%; Score 331; DB 10; Length 435;  
Best Local Similarity 85.1%; Pred. No. 2e-82;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCGCCACCCACC 60  
DB 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCGCCACCCACC 60  
QY 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
DB 61 CGCTCGCCACCCAGCCCGCCAGCAGCCGCTGGGAGCATGTAATGCCATCCAGGAGGCCCG 120  
QY 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAAACAGTAGAAGTCGTC 180  
DB 121 CGTCTCTCTGAAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATC 180

QY	181	TCTGAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA	240
Db	181	TCGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCTCGAGCTGTACAAG	240
QY	241	CAGGGCTTGGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCACGCCAC	300
Db	241	CAGGGCTTGGGGCAGCCTCACCAGCTCAAGGCCCTTGACCATGATGCCACGCCAC	300
QY	301	TACAAGCAGCACTGCCCCCACCCTCGAAACTTCTGTGCAACCCAGATGATCACCTTC	360
Db	301	TACAAGCAGCACTGCTTCCAAACCCGGAACCTTCTGTGCAACCCAGATTATCACTTT	360
QY	361	AAAAGTTTCAAAAAGAACCTCGAAGATTTCCTGTTTGAGATCCCGTTTGACTGCTGGAAG	420
Db	361	GAAAGTTTCAAAAGAACCTCGAAGACTTTCCTGCTTGTGTCATCCCTTTTGACTGCTGGAG	420
QY	421	CCAGCCCAGAGTAA	435
Db	421	CCAGTCCAGGAGTGA	435
RESULT	15		
ADN49689			
ID	ADN49689	standard; DNA; 435 BP.	
XX			
AC	ADN49689;		
XX			
DT	15-JUL-2004	(first entry)	
XX			
DE	Human granulocyte-macrophage colony stimulating factor DNA SeqID 17.		
XX			
KW	human; gene; ds; erythropoietin; EPO; glycoconjugation;		
KW	glycoPEGylated EPO peptide; anaemia; antianaemic; haematocrit level;		
KW	kidney dialysis; haematology;		
XX	granulocyte-macrophage colony stimulating factor.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2004033651-A2.		
XX			
PD	22-APR-2004.		
XX			
PF	08-OCT-2003; 2003WO-US031974.		
XX			
XX	09-OCT-2002; 2002WO-US032263.		
PR	05-NOV-2002; 2002US-00287994.		
PR	06-JAN-2003; 2003US-00360770.		
PR	19-FEB-2003; 2003US-00360779.		
PR	09-APR-2003; 2003US-00410945.		
XX			
PA	(NEOS-) NEOSE TECHNOLOGIES INC.		

CC	humans i.e. increasing the relative volume of blood occupied by
CC	erythrocytes. Furthermore, EPO therapy can be used to treat kidney
CC	dialysis patients. This polynucleotide is a human DNA sequence related to
CC	the field of haematology, given in an exemplification of the invention.
XX	
SQ	Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;
	Query Match           76.1%; Score 331; DB 12; Length 435;
	Best Local Similarity   85.1%; Pred. No. 2e-82;
	Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY	1 ATGTGGCTGCAGAAACCTGCTCTTCTTGGGCACATGTGGTTTACAGCATGCCCGCACCCACC 60 
DB	1 ATGTGGCTGCAGAGCCTGCTCTCTTGGGCACATGTGGCTTGCAGCATCTCTGCACCCGCC 60 
QY	61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120 
DB	61 CGCTGCCCCAGCCCCAGCAGCGACGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG 120 
QY	121 AGCCCTTCTGAACAACAGTAGTAGACACTGCTGTCCTATCATGAATGAAAACAGTAGAAGTGC 180 
DB	121 CGTCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATC 180 
QY	181 TCTGAAACGTTTTCAGCGCGGAGGAGCTGACATGCTGCGAGACTCGCCTGAGAGCTGTACAAA 240 
DB	181 TCAGAAATGTTTGACCTCCAGSAGCCGACCTGCTACAGACCCGCCCTGGAGCTGTACAAG 240 
QY	241 CAGGGCTTGGGGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCAC 300 
DB	241 CAGGGCTTGGGGGGCAGCCTCACCAGCTCAAGGGCCCCCTTGACCATGATGGCCAGCCAC 300 
QY	301 TACAAGGAGCACTGCCCCCCCACCTCTGGAACCTTCTGTGCGCAACCCAGATGATCACCTTC 360 
DB	301 TACAAGCAGCACTGCCCCCTCCAACCCCGGAACCTTCTGTGTCMAACCCAGATTATCACCTTT 360 
QY	361 AAAAGTTTCAAAAGAACCTGAAGGATTTTCTGTTTTGAGATCCCGTTTGACTGCTGGAAG 420 
DB	361 GAAGTTTCAAAGAGAACCTGAAGGACTTCTGCTGTGCATCCCTTTGACTGCTGGAG 420 
QY	421 CCAGCCGAGAGTAA 435
DB	421 CCAGTCCAGGAGTGA 435

Search completed: May 26, 2006, 00:41:08  
Job time : 451 secs

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 01:26:24 ; Search time 132 Seconds  
(without alignments)  
372.005 Million cell updates/sec

Title: US-10-614-481-8  
Perfect score: 435  
Sequence: 1 atgtggctgcagaacctgct.....ggaagccagccagaagtaa 435

Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA\_New.\*  
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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	331	76.1	435	7	US-11-183-218-17
2	331	76.1	781	6	US-10-511-937-396
3	38.8	8.9	50	6	US-10-511-937-64
4	36.4	8.4	1109	6	US-10-468-193-113
5	33.8	7.8	2139	7	US-11-293-697-965
6	33.8	7.8	2243	7	US-11-293-697-1196
7	33.8	7.8	2562	7	US-11-293-697-1692
8	33.6	7.7	2062	7	US-11-293-697-1541
9	33.4	7.7	1628	6	US-10-953-349-35010
10	32.6	7.5	4611	7	US-11-267-871-717
11	32.6	7.5	4844	1	US-09-484-331-19
12	32.6	7.5	5247	1	US-09-484-331-20
13	32.6	7.5	5264	6	US-10-485-397-10
14	32.6	7.5	5314	1	US-09-484-331-27
15	32.6	7.5	5408	6	US-10-485-397-9
16	32.6	7.5	5715	7	US-11-258-392-4
17	32.6	7.5	7873	6	US-10-485-397-7
18	32.6	7.5	7943	6	US-10-485-397-8
19	32.6	7.5	9737	1	US-09-484-331-22
20	32.6	7.5	9737	1	US-09-484-331-23
21	32.6	7.5	9737	1	US-09-484-331-28
22	32.6	7.5	9871	1	US-09-484-331-24
23	32.6	7.5	10060	1	US-09-484-331-25
24	32.2	7.4	1973	6	US-10-505-928-462
25	32	7.4	3972	7	US-11-293-697-1765

26	31.8	7.3	1548	6	US-10-953-349-27676	Sequence 27676, A
c 27	31.6	7.3	5133	6	US-10-511-937-2799	Sequence 2799, A
28	31	7.1	632	6	US-10-953-349-28960	Sequence 28960, A
29	31	7.1	634	6	US-10-953-349-25300	Sequence 25300, A
c 30	31	7.1	3316	6	US-10-981-760-2	Sequence 2, Appli
c 31	31	7.1	3331	6	US-10-953-349-8124	Sequence 8124, Ap
c 32	31	7.1	4644	1	US-09-484-331-19	Sequence 19, Appl
c 33	31	7.1	5247	1	US-09-484-331-20	Sequence 20, Appl
c 34	31	7.1	5314	1	US-09-484-331-27	Sequence 27, Appl
c 35	31	7.1	6084	1	US-09-484-331-7	Sequence 7, Appli
c 36	31	7.1	6085	1	US-09-484-331-8	Sequence 8, Appli
c 37	31	7.1	6086	1	US-09-484-331-9	Sequence 9, Appli
c 38	31	7.1	6629	6	US-10-946-650-49	Sequence 49, Appl
c 39	31	7.1	6836	1	US-09-484-331-18	Sequence 18, Appl
c 40	31	7.1	8540	7	US-11-183-218-57	Sequence 57, Appl
41	31	7.1	8687	7	US-11-297-317-15	Sequence 15, Appl
42	31	7.1	8687	7	US-11-297-317-16	Sequence 16, Appl
c 43	31	7.1	9209	7	US-11-183-218-58	Sequence 58, Appl
44	31	7.1	9362	7	US-11-297-317-18	Sequence 18, Appl
45	31	7.1	9400	7	US-11-297-317-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-11-183-218-17  
; Sequence 17, Application US/11183218  
; Publication No. US20060088906A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bowe, Caryne  
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND  
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN  
; FILE REFERENCE: 040853-01-5083-US02  
; CURRENT APPLICATION NUMBER: US/11/183,218  
; PRIOR FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US 10/410,945  
; PRIOR FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: PCT/US02/32263  
; PRIOR FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: US 60/334,301  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/334,233  
; PRIOR FILING DATE: 2001-11-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 435  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-183-218-17

Query Match 76.1%; Score 331; DB 7; Length 435;  
Best Local Similarity 85.1%; Pred. No. 2.8e-85;

	Matches	370;	Conservative	0;	Mismatches	65;	Indels	0;	Gaps	0;
Qy	1	ATGTGGCTGCAGAACCTGCTCTTCTTCCTGGCAGCTGTGGTTTACAGCATGCCCGCACCCACC	60							
Dd	1	ATGTGGCTGCAGAGCCGTGCTCTTGCGCACTGTGGCACTCTCTGCACCCGCC	60							
Qy	61	CGCCAAACCCAGCCCTGTCACTCGCGCCCTGGCAGCATGTGGATGGCATCAAGGAGGCCCTG	120							
Dd	61	CGCTCGCCAGCCCGCAGCAGCCCTTGGAGCATGTGAATGCATCCAGGAGGCCCGG	120							
Qy	121	AGCCCTTCTGAACAAACAGTAGTGCACACTGCTCTATCATGAATGAAAACAGTAGAAGTCCTC	180							
Dd	121	CGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATC	180							
Qy	181	TCTGAACAGTTTGAAGCGGAGGAGCTGACATGCTCTGCAGACTCGCTGGAAGCTGTACAA	240							
Dd	181	TCGAAAAATTGTTGACCTCCAGGAGCCGACCTGCGCTACAGACCCGCTGGAGCTGTACAAG	240							
Qy	241	CAGGGCTTTCGGGGCAGGCTCATCAAAGCTCGAAGGCCCTTGAACATGATGCCACAGCCAC	300							
Dd	241	CAGGGCTTCGGGGCAGGCTCACCAAGCTCAAAGGGCCCCCTTGACCATGATGCCACAGCCAC	300							
Qy	301	TACAAGCAGCACTGCCCCCCCACCCTCTGGAAAATTCTCTGTGTGCAACCCGAGATGATCACTTC	360							
Dd	301	TACAAGCAGCACTGCCCTCCAAACCCGGAATCTCTCTGTGTGCAACCCGAGATGATCACTTC	360							
Qy	361	AAAAAGTTTCAAAAAGAACCCTGAAGATTTCTGTGTTTGAGATCCCGTTTGTACTGCTGGGAG	420							
Dd	361	GAAGAATTTCAAGAAGAACCTGAAGACATTTCTGCTTGTCTATCCCCTTTGACTGCTGGAG	420							
Qy	421	CCAGCCCAAGATAA	435							
Dd	421	CCAGTCCAGGAGTGA	435							

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RESULT 2
US-10-511-937-396
; Sequence 396, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511.937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 396
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-396

Query March 76.1%; Score 331; DB 6; Length 781;
Best Local Similarity 85.1%; Pred. No. 3.5e-85;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0
1 ATGTGGGTGCAGAACTGTTCTTCTTGGGCACGTGTGGTTTACAGCATCCCGCACCCACC 60

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Db	33	ATGTGGCTGCAGAGCCTGCTGCTCTTTGGGCACTGTGGGCTGCAGCATCTCTGCACCCGGC	97
Qy	61	CGCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120
Db	93	CGCTCGCCAGCCCCAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCG	152
Qy	121	AGCCTTCTGAACAACAGTAGTGCACATGCTGCTATCATGAATGAACACGTAGAAGTCGTC	180
Db	153	CGTCTCTCTGAACCTGTAGTAGAGACACTGCTGCTGAGATGAATGAACACGTAGAAGTCATC	212
Qy	181	TCTGAACGTTTGACGCCGAGGAGCTGCATGCTCTGCAGACTCGCTGAAGCTGTACAAA	240
Db	213	TCAGAAATGTTTGACCTCCAGAGCCGACCTGCCTACAGACCCGCTGGAGCTGTACAAG	272
Qy	241	CAGGCTTGCGGGAGGAGCCTCATCAAGCTCGAAGGCCCTTGAACCATGATGGCAGCCAC	300
Db	273	CAGGCTTGCGGGAGGAGCCTCACCAAGCTCAAGGGCCCTTGAACCATGATGGCAGCCAC	332
Qy	301	TACAGCAGCACTGCCCCCCCAGCCCTCGAACTTCTCTGTGCAACCCAGATGATCACCTTC	360
Db	333	TACAGCAGCACTGCCCTTCCAAACCCCGAACTTCTGTGCAACCCAGATGATCACCTTC	392
Qy	361	AAAAAGTTTCAAAAAGAACCTCGAAGATTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG	420
Db	393	GAAAGTTTCAAAGAGAACCTCGAAGACTTTCTGCTGTGTATCCCCCTTTCAGCTGCTGGAG	452
Qy	421	CCAGCCCAAGATGA 435	
Db	453	CCAGTCCAGGAGTGA 467	
RESULT 3			
US-10-511-937-64			
; Sequence 64, Application US/10511937			
; Publication No. US20060088836A1			
; GENERAL INFORMATION:			
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.			
; APPLICANT: Wohlgenuth, Jay			
; APPLICANT: Fry, Kirk			
; APPLICANT: Woodward, Robert			
; APPLICANT: Ly, Ngoc			
; APPLICANT: Prentice, James			
; APPLICANT: Morris, MacDonald			
; APPLICANT: Rosenberg, Steven			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING			
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION			
; FILE REFERENCE: 506612000104			
; CURRENT APPLICATION NUMBER: US/10/511,937			
; CURRENT FILING DATE: 2004-10-19			
; PRIOR APPLICATION NUMBER: PCT/US2003/012946			
; PRIOR FILING DATE: 2003-04-24			
; PRIOR APPLICATION NUMBER: US 10/131,831			
; PRIOR FILING DATE: 2002-04-24			
; PRIOR APPLICATION NUMBER: US 10/325,899			
; PRIOR FILING DATE: 2002-12-20			
; NUMBER OF SEQ ID NOS: 3117			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 64			
; LENGTH: 50			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-511-937-64			

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Query Match      8.9%; Score 38.8; DB 6; Length 50;
Best Local Similarity 86.0%; Pred. No. 0.009;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0
OY 316 CCCCCCACCCTGGAAACTTCCTGTGCACCCAGATGATCACCCTTCAAAAG 365
      |||||
Db 1 CCTCCACCCCGGAAACTTCCTGTGCACCCAGACTATCACCCTTGAAG 50

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Matches	71;	Conservative	0;	Mismatches	62;	Indels	0;	Gaps
QY	196	GCCGAGGCTGACATGCGCTCGAGACTCGCTGAAAGCTGTACAAACAGGGCTTGCGGGC	255					

196 GCGGAGAGCTGACATGCTCGAGACTCGCCTGAAGCTGTACAAACAGGCTTGGCGGGC 255

Qy	196	GCCGAGGAGCTGACATGCTCTGACACTCCCTGAAGCTTACAAACAGGCTTTCGGGGC	255
Dβ	1422	GCGGGGAGGCCGAGGCTGTAGCTTGACAGCAGCTCAAGGCGCTTGGGTCCCCCC	1361

Db 1846 GCCGGGAGCCCGAGGCTGTAGCTGCAGCAGCTGCRAAGGGCCCTGGGTCCCCCCC 1787  
QY 256 AGCTTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCAGCACTACAAGCAGCACTGC 315  
Db 1786 GGCCCCATCAGCACCAGCGGCGAGCAGCTGATGACGCTGCAGCGCCACGTGCAGGGCTGT 1727  
QY 316 CCCCCCAGCCCTGG 328  
Db 1726 GTCCCCCTCCTCG 1714

## RESULT 8

US-11-293-697-1541/c  
; Sequence 1541, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1541  
; LENGTH: 2062  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-293-697-1541

Query Match 7.7%; Score 33.6; DB 7; Length 2062;  
Best Local Similarity 52.9%; Pred. No. 1.2;  
Matches 72; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 190 TTGTAGCGCGAGGAGTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAACAGGGCTTG 249  
Db 189 TTGGAGACTTCCCTGTGCTGTGTCGTGTCGATGGGTGAAGCGTGCAGATGGCTTTG 130  
QY 250 CGGGCAGCCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCAGCCACTACAAAGCAG 309  
Db 129 AGCAGCTCCTCTTCAAGCTCCCATGCGCGGCGCCTGTGCCCGGCCCAACCCCTCCTG 70  
QY 310 CACTGCCCCCCCCACCC 325  
Db 69 CCCAGCCAGCCCTCC 54

## RESULT 9

US-10-953-349-35010  
; Sequence 35010, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 35010  
; LENGTH: 1628  
; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-35010

Query Match 7.7%; Score 33.4; DB 6; Length 1628;  
Best Local Similarity 53.4%; Pred. No. 1.2;  
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
QY 185 AAACCTTTGACCGCCGAGGAGTGACATGCTGCAGATCGCCTGAAGCTGTACAAACAGG 244

Db 1107 AGACGAACGCGCGGGGAGAGATGTATCCAGACGCGCATGCGGAGTACAAGAGG 1166  
QY 245 GCTTGGGGGAGAGCTTATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCACTACA 304  
Db 1167 AGCTGTGGGAGTGCTCAAGAAGGAGCAACACCTCTACTATGTGCGGGCTCAAGGGCA 1226  
QY 305 AGCAGCACTGC 315  
Db 1227 TGGAGAGGGC 1237

## RESULT 10

US-11-267-871-717  
; Sequence 717, Application US/11267871  
; Publication No. US20060094655A1  
; GENERAL INFORMATION:  
; APPLICANT: Guyon, Thierry  
; APPLICANT: Borrelly, Gilles  
; APPLICANT: Drittanti, Lila  
; APPLICANT: Vega, Manuel  
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES  
; FILE REFERENCE: 17109-015001/925  
; CURRENT APPLICATION NUMBER: US/11/267,871  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: 60/706,697  
; PRIOR FILING DATE: 2005-08-08  
; PRIOR APPLICATION NUMBER: 60/625,652  
; PRIOR FILING DATE: 2004-11-04  
; NUMBER OF SEQ ID NOS: 719  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 717  
; LENGTH: 4611  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pTOPO hGH vector  
US-11-267-871-717

Query Match 7.5%; Score 32.6; DB 7; Length 4611;  
Best Local Similarity 48.2%; Pred. No. 3.1;  
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;  
QY 139 AGTGACACTGCTGTATCATGAATGAAACAGTAGAAGTGTCTCTGAAACGTTTCACGCGC 198  
Db 2188 AGAAAGCGGCCATTTCCACCATGATATTCCGGAAGCAGGATCGCCATGGGTACAGAC 2247  
QY 199 GAGGAGCTGACATGCTGCAGACTCGCTGAAGCTGTACAAACAGGGCTTGGGGGCGAGC 258  
Db 2248 GAGATCCTCGCGCTCGGGCATGCTCGCTTGAGCCTGGCGAACAGTTCCGCTGGCGCGAG 2307  
QY 259 CTCATCAAGCTCGAAGGGCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCC 318  
Db 2308 CCCCTGATGCTCTTCGTCAGATCATCTGTATCGCAAGACCGGCTTCATCCGAGTACG 2367  
QY 319 CCCACCTGGA 329  
Db 2368 TGCTCGCTCGA 2378

## RESULT 11

US-09-484-331-19  
; Sequence 19, Application US/09484331  
; Publication No. US20060105318A1  
; GENERAL INFORMATION:  
; APPLICANT: HARRINGTON, JOHN J.  
; APPLICANT: SHERF, BRUCE  
; APPLICANT: RUNDLETT, STEPHEN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF  
; TITLE OF INVENTION: ENDOGENOUS GENES  
; FILE REFERENCE: 0221-0003L  
; CURRENT APPLICATION NUMBER: US/09/484,331  
; CURRENT FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: 09/276,820

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; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-331-19

Query Match      7.5%; Score 32.6; DB 1; Length 4644;
Best Local Similarity 48.2%; Pred. No. 3.1;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 139 AGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTGTCTCTGAAACGTTTGACGCC 198
Db 2314 AGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTACGAC 2373

QY 199 GAGGAGCTGACATGCTCGAGACTCGCCTGAAAGCTGTACAAACAGGGCTTGCGGGCGCAGC 258
Db 2374 GAGATCCTCGCGCTCGGCATGCTCGCCTTGAGCCTGGGACACATGTCGGCTGGCGCGAG 2433

QY 259 CTCATCAAGCTCGAAGGCGCCCTTGACCATGTATGATGGCCAGCCACTACAAGCAGCACTGCCCC 318
Db 2434 CCCCTGATGCTTCTCGTCCAGATCATCTCTGATCGACAAAGACCGGCTTCCATCCGAGTACG 2493

QY 319 CCCACCCCTGGA 329
Db 2494 TGCTCGCTCGA 2504

RESULT 12
US-09-484-331-20
; Sequence 20, Application US/09484331
; Publication No. US20060105318A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003L
; CURRENT APPLICATION NUMBER: US/09/484,331
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-331-20

Query Match      7.5%; Score 32.6; DB 1; Length 5247;
Best Local Similarity 48.2%; Pred. No. 3.2;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 139 AGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTGTCTCTGAAACGTTTGACGCC 198
Db 2740 AGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTACGAC 2681

QY 199 GAGGAGCTGACATGCTCGAGACTCGCCTGAAAGCTGTACAAACAGGGCTTGCGGGCGCAGC 258
Db 2680 GAGATCCTCGCGCTCGGCATGCTCGCCTTGAGCCTGGGAAACAGTTTCGGCTGGCGCGAG 2621

QY 259 CTCATCAAGCTCGAAGGCGCCCTTGACCATGTATGATGGCCAGCCACTACAAGCAGCACTGCCCC 318
Db 2620 CCCCTGATGCTTCTCGTCCAGATCATCTCTGATCGACAAAGACCGGCTTCCATCCGAGTACG 2561

QY 319 CCCACCCCTGGA 329
Db 2560 TGCTCGCTCGA 2550

RESULT 14
US-09-484-331-27
; Sequence 27, Application US/09484331
; Publication No. US20060105318A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003L
; CURRENT APPLICATION NUMBER: US/09/484,331
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 08/941,223
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-331-27

Query Match      7.5%; Score 32.6; DB 6; Length 5264;
Best Local Similarity 48.2%; Pred. No. 3.2;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 139 AGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTGTCTCTGAAACGTTTGACGCC 198
Db 2740 AGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTACGAC 2681

QY 199 GAGGAGCTGACATGCTCGAGACTCGCCTGAAAGCTGTACAAACAGGGCTTGCGGGCGCAGC 258
Db 2680 GAGATCCTCGCGCTCGGCATGCTCGCCTTGAGCCTGGGAAACAGTTTCGGCTGGCGCGAG 2621

QY 259 CTCATCAAGCTCGAAGGCGCCCTTGACCATGTATGATGGCCAGCCACTACAAGCAGCACTGCCCC 318
Db 2620 CCCCTGATGCTTCTCGTCCAGATCATCTCTGATCGACAAAGACCGGCTTCCATCCGAGTACG 2561

QY 319 CCCACCCCTGGA 329
Db 2560 TGCTCGCTCGA 2452

RESULT 13
US-10-485-397-10/c
; Sequence 10, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTANA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B697USPCT01
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 5264
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pSEAPstopneo is a circular Plasmid DNA
US-10-485-397-10

Query Match      7.5%; Score 32.6; DB 6; Length 5264;
Best Local Similarity 48.2%; Pred. No. 3.2;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 139 AGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTGTCTCTGAAACGTTTGACGCC 198
Db 2740 AGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTACGAC 2681

QY 199 GAGGAGCTGACATGCTCGAGACTCGCCTGAAAGCTGTACAAACAGGGCTTGCGGGCGCAGC 258
Db 2680 GAGATCCTCGCGCTCGGCATGCTCGCCTTGAGCCTGGGAAACAGTTTCGGCTGGCGCGAG 2621

QY 259 CTCATCAAGCTCGAAGGCGCCCTTGACCATGTATGATGGCCAGCCACTACAAGCAGCACTGCCCC 318
Db 2620 CCCCTGATGCTTCTCGTCCAGATCATCTCTGATCGACAAAGACCGGCTTCCATCCGAGTACG 2561

QY 319 CCCACCCCTGGA 329
Db 2442 TGCTCGCTCGA 2452
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; PRIOR APPLICATION NUMBER: 09/263,814  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/253,022  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/159,643  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/941,223  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 5314  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-484-331-27

Query Match 7.5%; Score 32.6; DB 1; Length 5314;  
Best Local Similarity 48.2%; Pred. No. 3.3;  
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;  
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Db |||||  
Db 2329 AGAAAGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATGCCCATGGGTCCAGCAG 2388  
QY 199 GAGGAGCTGACATGCTCGAGACTCGCCTGAGCTGTACAAACAGGGCTTGCGGGGCAGC 258  
Db |||||  
Db 2389 GAGATCCTCGCGTCGGGCATGCTCGCCTTGAGCCTTGGCGAACAGTTTCGGCTGGCGCGAG 2448  
QY 259 CTCATCAAGCTCGAAGGCCCTTTGACCATGATGGCCAGCCTACAAAGCAGCAGCTGCCCCC 318  
Db |||||  
Db 2449 CCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTAGC 2508  
QY 319 CCCACCCTGGA 329  
Db |||||  
Db 2509 TGCTCGCTCGA 2519

RESULT 15  
US-10-485-397-9/c  
; Sequence 9, Application US/10485397  
; Publication No. US2006009673A1  
; GENERAL INFORMATION:  
; APPLICANT: ALTANA Pharma AG  
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method  
; FILE REFERENCE: B697USPT01  
; CURRENT APPLICATION NUMBER: US/10/485,397  
; CURRENT FILING DATE: 2004-01-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 5408  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: pSEAPstopMneo is a circular Plasmid DNA  
US-10-485-397-9

Query Match 7.5%; Score 32.6; DB 6; Length 5408;  
Best Local Similarity 48.2%; Pred. No. 3.3;  
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;  
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Db |||||  
Db 2884 AGAAAGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATGCCCATGGGTCCAGCAG 2825  
QY 199 GAGGAGCTGACATGCTCGAGACTCGCCTGAAAGCTGTACAAACAGGGCTTGCGGGGCAGC 258  
Db |||||  
Db 2824 GAGATCCTCGCGTCGGGCATGCTCGCCTTGAGCCTGGCGAACAGTTTCGGCTGGCGCGAG 2765  
QY 259 CTCATCAAGCTCGAAGGCCCTTTGACCATGATGGCCAGGCCACTACAAAGCAGCAGCTGCCCCC 318  
Db |||||  
Db 2764 CCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTAGC 2705

QY 319 CCCACCCTGGA 329  
Db 2704 TGCTCGCTCGA 2694  
Search completed: May 26, 2006, 01:31:24  
Job time : 133 secs

GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 00:46:33 ; Search time 3394 Seconds  
(without alignments)  
7167.033 Million cell updates/sec

Title: US-10-614-481-8  
Perfect score: 435  
Sequence: 1 atgtggctgcgaactgtct.....ggaagccagccaggaagtaa 435

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	76.1	435	14	DQ053415 Homo sapi
2	331	76.1	588	7	AW207707 UI-H-BI2-
3	331	76.1	660	7	BE218982 hv47a07.x
4	331	76.1	666	1	AI912784 wel1f07.x
5	331	76.1	672	7	BE671554 7e53h07.x
6	331	76.1	695	7	BE669962 7e27g08.x
7	329.4	75.7	435	14	DQ053416
8	329.4	75.7	584	5	CF341802 TgESTzy14
9	329	75.6	895	7	BE873976 601484045
10	323	74.3	585	5	CF370833 TgESTzy15
11	323	74.3	592	5	CF370966 TgESTzy15
12	319	73.3	658	4	BX111836 EX111836
13	318.2	73.1	561	4	CB457551 714908 MA
14	318.2	73.1	572	2	BM539160 hb05e10.g
15	315.2	72.5	672	5	CF614774 CES009198
16	310.6	71.4	565	2	BF938995 7r03f11.x
17	308.6	70.9	511	4	CB430266 606148 MA
18	300.2	69.0	488	8	CV700569 TgESTzy85
19	292.2	67.2	423	7	AW784714 zb77g08.g

c 20	283	65.1	718	5	CD369973	UI-H-FT1-
c 21	272.2	62.6	701	3	BU633411	UI-H-FL1-
c 22	271	62.3	475	1	AA995402	or74f05.a
c 23	264.8	60.9	388	10	DV799573	est.t.tru
c 24	258	59.3	666	4	CA307828	UI-H-FT1-
c 25	244.2	56.1	661	5	CD368851	UI-H-FT1-
c 26	233.6	53.7	336	7	AW951121	EST363191
c 27	219.8	50.5	1034	6	AK053196	Mus muscu
c 28	208.8	48.0	608	5	CD367244	UI-H-FT2-
c 29	183.6	42.2	549	1	AI677936	wc88f12.x
c 30	179.8	41.3	274	1	AA361936	EST71529
c 31	179.8	41.3	629	7	BB664267	BB664267
c 32	176.2	40.5	531	2	BG236310	naif26a07.
c 33	167.8	38.6	631	9	DN753142	GL-CF-993
c 34	149.6	34.4	647	7	BB533718	BB533718
c 35	139.8	32.1	269	5	CF370885	TgESTzy15
c 36	137.4	31.6	244	2	BG236058	naif21h12.
c 37	134.2	30.9	517	4	CB430980	606916 MA
c 38	123	28.3	483	1	AI180669	uc47d08.x
c 39	122.4	28.1	369	4	BX521029	BX521029
c 40	112.8	25.9	470	1	AI121878	ud13c11.x
c 41	108	24.8	488	9	DN505558	HL01015B1
c 42	106.2	24.4	697	14	AG112609	Pan trogl
c 43	103	23.7	678	9	DR004241	TC124014
c 44	96	22.1	160	5	CF341980	TgESTzy15
c 45	88.6	20.4	136	5	CF341168	TgESTzy14

## ALIGNMENTS

RESULT 1	DQ053415	435 bp	DNA	linear	GSS 02-JUN-2005
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DEFINITION	Homo sapiens	HC14003	gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION	DQ053415	435 bp	DNA	linear	GSS 02-JUN-2005
VERSION	DQ053415.1	GI:66899362			
KEYWORDS	GSS.				
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 435)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	A scan for positively selected genes in the genomes of humans and chimpanzees				
JOURNAL	(er) PLoS Biol. 3 (6), E170 (2005)				
PUBMED	15869325				
REFERENCE	2 (bases 1 to 435)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submissio				
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
	/chromosome="5"				
gene	<1..>435				
	/locus_tag="HC14003"				
ORIGIN					
Query Match	76.1%	Score	331	DB	14
					Length 435

Best Local Similarity 85.1%; Pred. No. 5.7e-83;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTCTCTTCTTGGGCACTGTGGTTTACAGCATCCGCCACCCACC 60  
Db 1 ATGTGGCTGCAGAGCTCTCTCTTGGGCACTGTGGGCTGCAGCATCTCTGCACCCGCC 60

QY 61 CGCCMCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
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QY 121 AGCCTTCTGAACAAAGTAGTGACACTCTGCTATCATGAATGAACAGTAGTGAAGTCCT 180  
Db 121 CGTCTCTGAACCTGAGTAGAGACTCTGCTGTGATGAATGAACAGTAGTGAAGTCATC 180

QY 181 TCTGAACAGTTTGACGCGGAGGAGCTGCATCGCTGCGAGACTCGCTCAAGCTGTACAAA 240  
Db 181 TCAGAAATGTTTGACCTCCAGGAGCGGACCTGCCTACAGACCCGCTGGAGCTGTACAA 240

QY 241 CAGGCTTTCGGGGGAGCCTCATCAAGCTCGAGGCCCTTGACCATGATGCCAGCCAC 300  
Db 241 CAGGCTTTCGGGGGAGCCTCACCAAGCTCAAGGCCCTTGACCATGATGCCAGCCAC 300

QY 301 TACAGCAGCACTGCCGCCGCCCTCGAACTTCTGTGCAACCCAGATGATCACCTTC 360  
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QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAAG 420  
Db 361 GAAAGTTTCAAAAGAACTGAAGGACTTTCTGTGTTGATCCCTTTGACTGTGCGGAG 420

QY 421 CCAGCCGAGAGTAA 435  
Db 421 CCAGTCCAGGAGTGA 435

RESULT 2  
AW207707  
LOCUS UI-H-B12-age-e-09-0-UI-s1 NCI\_CGAP\_Sub4 Homo sapiens cDNA clone  
DEFINITION IMAGE:2724184 3', mRNA sequence.  
ACCESSION AW207707  
VERSION AW207707.1 GI:6507203  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo;  
1 (bases 1 to 588)  
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Oligo-dT track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.B.  
Soares Lab Clone distribution: NCI-CGAP clone distribution  
information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward  
POLYA=No.

Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone\_lib="NCI CGAP Sub4"  
/note="Vector: pT7T3D-PacI; Site 1: Not 1; Site 2: Eco RI;  
The NCI\_CGAP\_Sub4 library is a subtracted library derived

FEATURES  
source

from the NCI CGAP Sub2 library which is a subtracted library derived from the NCI\_CGAP\_Sub1 library, which is a subtracted library derived from B1. B1 constitutes a mixture of 21 normalized or subtracted NCI\_CGAP libraries: NCI\_CGAP\_Co4, NCI\_CGAP\_Pr22, NCI\_CGAP\_Pr28, NCI\_CGAP\_Co10, NCI\_CGAP\_Co16, NCI\_CGAP\_Kid5, NCI\_CGAP\_Kid12, NCI\_CGAP\_Kid3, NCI\_CGAP\_Kid11, NCI\_CGAP\_Lym2, NCI\_CGAP\_Br2, NCI\_CGAP\_Co8, NCI\_CGAP\_CLL1, NCI\_CGAP\_Le12, NCI\_CGAP\_Brn23, NCI\_CGAP\_Lu5, NCI\_CGAP\_Lu24, NCI\_CGAP\_Lu19, NCI\_CGAP\_GC4, NCI\_CGAP\_GC6, NCI\_CGAP\_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:  
NCI\_CGAP\_Kid3 pool 1 : LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonids 132376-1323911, 1456008-1456775, 1500552-1502855) NCI\_CGAP\_Kid5 pool 1 : LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonids 1323912-1325831, 1471368-1472903, 1492104-1493255)  
NCI\_CGAP\_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE Clonids 1414920-1417991, 1520904-1522439) NCI\_CGAP\_GC4 pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonids 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI\_CGAP\_Pr22 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonids 985608-986759, 1101192-1101959, 1217928-1220615) NCI\_CGAP\_Co10 pool 1 : LLAM 2844-2853, 2871-2872 (IMAGE Clonids 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996) : Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]  
TAG\_TISSUE=colon  
TAG\_LIB=NCI\_CGAP\_Co4  
TAG\_SEQ=CTTCG\*

ORIGIN

Query Match 76.1%; Score 331; DB 7; Length 588;  
Best Local Similarity 85.1%; Pred. No. 6.2e-83;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTCTCTTCTTGGGCACTGTGGTTTACAGCATCCGCCACCCACC 60  
Db 37 ATGTGGCTGCAGAGCTCTCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 96

QY 61 CGCCMCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
Db 97 CGCTCGCCCGAGCCCGAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCG 156

QY 121 AGCCTTCTGAACAAAGTAGTGACACTCTGCTATCATGAATGAACAGTAGTGAAGTCCT 180  
Db 157 CGTCTCTGAACCTGAGTAGAGACTCTGCTGTGATGAATGAACAGTAGTGAAGTCATC 216

QY 181 TCTGAACAGTTTGACGCGGAGGAGCTGCATGCCTTGCAGACTCGCTGAAGCTGTACAAA 240  
Db 217 TCAGAAATGTTTGACCTCCAGGAGCGGACCTGCCTTACAGACCCGCTGGAGCTGTACA 276

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QY 301 TACAGCAGCACTGCCGCCGCCCTCGAACTTCTGTGCAACCCAGATGATCACCTTC 360  
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QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAAG 420  
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QY 421 CCAGCCGAGAGTAA 435  
Db 457 CCAGTCCAGGAGTGA 471



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LOCUS
DEFINITION
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    FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    BE218982.1 GI:8906300
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ORGANISM
    Homo sapiens
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    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
REFERENCE
    1 (bases 1 to 660)
    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
    Tumor Gene Index
JOURNAL
COMMENT
    Unpublished (1997)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
    Emmert-Buck, M.D., Ph.D.
    cDNA Library Preparation: M. Bento Soares, Ph.D.
    cDNA Library Arrayed by: Greg Lennon, Ph.D.
    DNA Sequencing by: Washington University Genome Sequencing Center
    Clone distribution: NCI-CGAP clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL, send email to:
    info@image.llnl.gov
    Seq primer: -40UP from Gibco
    High quality sequence stop: 445.
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    /note="Organ: lung; Vector: pTTT3D-PacI; Plasmid DNA from
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    circles were made in vitro. Following HAP purification,
    this DNA was used as tracer in a subtractive hybridization
    reaction. The driver was PCR-amplified cDNAs from a pool
    of 5,000 clones made from the same library (cloneIDs
    1414920-1417991 and 1520904-1522439). Subtraction by Bento
    Soares and M. Fatima Bonaldo."
    ORIGIN
    Query Match 76.1%; Score 331; DB 7; Length 660;
    Best Local Similarity 85.1%; Pred. No. 6.5e-83;
    Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
    QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
    DB 5 ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 64
    QY 61 CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAGAGAGCCCTG 120
    DB 65 CGCTCGCCAGCCCGCAGCAGCGAGCCCTGGGAGCATGTGAATGCCATCCAGGAGCCCGG 124
    QY 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTAAGTCGTC 180
    DB 125 CGTCTCTTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGTAAGTCATC 184
    QY 181 TCTGAACAGTTTGACCGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA 240
    DB 185 TCAGAAATGTTTGACCTCCAGGAGCCGACCTGCTTACAGACCCGCTGGAGCTGTACAG 244
    QY 241 CAGGGCTTCGGGGGAGGCGCTTATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
    DB 245 CAGGGCCTTCGGGGGAGGCGCTTACCAAGCTCAAGGGCCGCTTGACCATGATGCCAGCCAC 304

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QY 301 TACAAGCAGCACTGCCCCGCCACCTGGAAACTTCTGTGTCAACCCAGATGATCACCTTC 360
DB 305 TACAAGCAGCACTGCCCTCCACACCCCGGAAACTTCTGTGTCAACCCAGATGATCACCTTC 364
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTCTGTGTGAGATCCCGTTTGACTGCTGGAAG 420
DB 365 GAAAGTTTCAAAAGAAACCTGAAGGACTTCTGTGTGCTATCCCTTTGACTGCTGGAG 424
QY 421 CCAGCCCAAGAGTAA 435
DB 425 CCAGTCCAGGAGTGA 439
RESULT 4
LOCUS
DEFINITION
    AI912784 666 bp mRNA linear EST 18-DEC-1999
    we13f07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2340997 3'
    similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
    FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    AI912784.1 GI:5632639
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
REFERENCE
    1 (bases 1 to 666)
    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
    Tumor Gene Index
JOURNAL
COMMENT
    Unpublished (1997)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
    Emmert-Buck, M.D., Ph.D.
    cDNA Library Preparation: M. Bento Soares, Ph.D.
    cDNA Library Arrayed by: Greg Lennon, Ph.D.
    DNA Sequencing by: Washington University Genome Sequencing Center
    Clone distribution: NCI-CGAP clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    www-bio.llnl.gov/bbrp/image/image.html
    Insert Length: 743 Std Error: 0.00
    Seq primer: -40UP from Gibco
    High quality sequence stop: 447.
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    /lab_host="DH10B"
    /clone_lib="NCI CGAP Lu24"
    /note="Organ: lung; Vector: pTTT3D-PacI; Plasmid DNA from
    the normalized library NCI CGAP Lu5 was prepared, and as
    circles were made in vitro. Following HAP purification,
    this DNA was used as tracer in a subtractive hybridization
    reaction. The driver was PCR-amplified cDNAs from a pool
    of 5,000 clones made from the same library (cloneIDs
    1414920-1417991 and 1520904-1522439). Subtraction by Bento
    Soares and M. Fatima Bonaldo."
    ORIGIN
    Query Match 76.1%; Score 331; DB 1; Length 666;
    Best Local Similarity 85.1%; Pred. No. 6.5e-83;
    Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
    QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
    DB 5 ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 64

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QY 61 CGCCAAACCCAGCCCTGTCACTCGGCGCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
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Db 65 CGCTCGCCCGAGCCCGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 124  
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QY 121 AGCCTTCTGAACAACAGTAGTACACTGCTCTATCATGAATGAACAGTAGTAAGTCTGC 180  
|||  
Db 125 CGTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGTAAGTCTATC 184  
|||  
QY 181 TCTGAACAGTTTGAGCGCCGAGGAGTGACATGCCCTGCAGACTCGCCTGAAGCTGTACAAA 240  
|||  
Db 185 TCAGAAATGTTTGAACCTCCAGGAGCCGACCTGCCCTACAGACCCGCGCTGGAGCTGTACAA 244  
|||  
QY 241 CAGGCTTGCAGGCGAGCCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300  
|||  
Db 245 CAGGCGCTGCGGGGAGCCTCACCAAGCTCAAGGCGCCCTTGACCATGATGCCAGCCAC 304  
|||  
QY 301 TACAAGCAGCACTGCCCCCCCCCACTCTGTGAACTCTCTGTGCAACCCAGATGATCACTTC 360  
|||  
Db 305 TACAAGCAGCACTGCCCCCCCCCACTCTGTGAACTCTCTGTGCAACCCAGATGATCACTTC 364  
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QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGTAGATCCCGCTTTGACTGCTGGAAG 420  
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Db 365 GAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGTAGATCCCGCTTTGACTGCTGGAAG 424  
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QY 421 CCAGCCCGAAGTAA 435  
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Db 425 CCAGTCCAGGAGTGA 439  
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RESULT 5  
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LOCUS 7e53h07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3286237 3'  
DEFINITION similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING  
FACTOR PRECURSOR (HUMAN); mRNA sequence.

ACCESSION BE671554  
VERSION BE671554.1 GI:10032095  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo;  
1 (bases 1 to 672)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 440.

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/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lu24"  
/note="Organ: lung; Vector: pT7T3D-PacI; Plasmid DNA from  
the normalized library NCI CGAP Lu5 was prepared, and ss  
circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (clonoids  
1414920-1417991 and 1520941-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 75.1%; Score 331; DB 7; Length 672;  
Best Local Similarity 85.1%; Pred. No. 6.5e-83;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
QY 1 ATGTGGCTGCAGAAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATCCCGCACCCACC 60  
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Db 12 ATGTGGCTGCAGAGCCTGCTGCTTCTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCC 71  
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QY 61 CGCCAAACCCAGCCTGTCACTCGGCGCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
|||  
Db 72 CGCTCGCCCGAGCCCGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 131  
|||  
QY 121 AGCCTTCTGAACAACAGTAGTACACTGCTCTATCATGAATGAACAGTAGTAAGTCTGC 180  
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Db 132 CGTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGTAAGTCTATC 191  
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QY 181 TCTGAACAGTTTGAGCGCGAGGAGTGACATGCCCTGCAGACTCGCCTGAAGCTGTACAAA 240  
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Db 192 TCAGAAATGTTTGAACCTCCAGGAGCCGACCTGCCTACAGACCCGCGCTGGAGCTGTACAAG 251  
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QY 241 CAGGCTTGCAGGCGAGCCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300  
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Db 252 CAGGCGCTGCGGGGAGCCTCACCAAGCTCAAGGCGCCCTTGACCATGATGCCAGCCAC 311  
|||  
QY 301 TACAAGCAGCACTGCCCCCCCCCACTCTGTGAACTCTCTGTGCAACCCAGATGATCACTTC 360  
|||  
Db 312 TACAAGCAGCACTGCGCTTCCAAACCCCGAACTTCTGTGCAACCCAGATGATCACTTC 371  
|||  
QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGTAGATCCCGCTTTGACTGCTGGAAG 420  
|||  
Db 372 GAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGTAGATCCCGCTTTGACTGCTGGAAG 431  
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QY 421 CCAGCCCGAAGTAA 435  
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Db 432 CCAGTCCAGGAGTGA 446  
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RESULT 6  
BE669962  
LOCUS 7e27g08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3283742 3'  
DEFINITION similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING  
FACTOR PRECURSOR (HUMAN); mRNA sequence.

ACCESSION BE669962  
VERSION BE669962.1 GI:10030503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo;  
1 (bases 1 to 695)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco

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FEATURES
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    /clone="IMAGE:3283742"
    /tissue_type="carcinoid"
    /lab_host="DH10B"
    /clone_lib="NCI CGAP Lu24"
    /note="Organ: lung; Vector: pTT3D-PacI; Plasmid DNA from
the normalized library NCI CGAP Lu5 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
  Query Match      76.1%; Score 331; DB 7; Length 695;
  Best Local Similarity 85.1%; Pred. No. 6.6e-83;
  Matches 370; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
  QY 1 ATGTGGCTGCAGAACCTGCTCTTCTTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
  DB 41 ATGTGGCTGCAGAGCCTGCTGCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 100
  QY 61 CGCCAAACCCAGCCTGTCACTCGGCCCTGGGAGCATGTGGATGCCATCAAGAGGCCCTTG 120
  DB 101 CGCTCGCCAGCCCGCAGCAGCGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 160
  QY 121 AGCCTTCTGAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTAAGTCGTC 180
  DB 161 CGTCTCTGAACCTGAGTAGAGACTGCTGCTGAGATGAATGAACAGTAGTAAGTCATC 220
  QY 181 TCTGAAACGTTTGACGCGGAGGAGCTGACATGCTCGCTGCAGACTCGCCTGAAGCTGTACAA 240
  DB 221 TCAGAAATGTTTGACCTCCAGAGCCGACCTGCTCTACAGACCCGCTGGAGCTGTACAAG 280
  QY 241 CAGGCTTCGCGGGGAGGCTCATCAAGCTCGAGGCCCTTGACCATGATGCCAGCCAC 300
  DB 281 CAGGCTTCGCGGGGAGGCTCACCAGCTCAAGGCGCCCTTGACCATGATGCCAGCCAC 340
  QY 301 TACAGCAGCAGCTGCCCCCAGCCCTCGGAATCTCTGTGCAACCCAGATGATCACTTC 360
  DB 341 TACAAGCAGCAGCTGCCCCCAGCCCTCGGAATCTCTGTGCAACCCAGATGATCACTTC 400
  QY 361 AAAAGTTTCAAAAAGAACTTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAAG 420
  DB 401 GAAAGTTTCAAAAGAACTTGAAGGACTTTCTGTGTTGATCATCCCTTTGACTGTGGAG 460
  QY 421 CCAGCCCAAGATGA 435
  DB 461 CCAGTCCAGGAGTGA 475
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  DQ053416
  LOCUS
  DEFINITION
    Pan troglodytes HCl4003 gene, VIRTUAL TRANSCRIPT, partial sequence,
    genomic survey sequence.
  ACCESSION
    DQ053416
  VERSION
    DQ053416.1 GI:66899363
  KEYWORDS
    GSS.
  SOURCE
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  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Pan.
  REFERENCE
    1 (bases 1 to 435)
    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
    Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
    White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
    A Scan for Positively Selected Genes in the Genomes of Humans and
    Chimpanzees
    (er) PLOS Biol. 3 (6), E170 (2005)
    15869325
    2 (bases 1 to 435)
    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
    Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
    White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
    Direct Submission
    Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
    Rockville, MD 20850, USA
    COMMENT
    This sequence was made by sequencing genomic exons and ordering
    them based on alignment. Translation starts at the beginning of
    alignment.
  FEATURES
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    Best Local Similarity 84.8%; Pred. No. 1.6e-82;
    Matches 369; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
    QY 1 ATGTGGCTGCAGAACCTGCTCTTCTTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
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    QY 61 CGCCAAACCCAGCCTGTCACTCGGCCCTGGGAGCATGTGGATGCCATCAAGAGGCCCTTG 120
    DB 61 CGCTCGCCAGCCCGCAGCAGCGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120
    QY 121 AGCCTTCTGAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTAAGTCGTC 180
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    QY 241 CAGGCTTCGCGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
    DB 241 CAGGCTTCGCGGGGAGGCTCACCAGCTCAAGGCTCAAGGCCCTTGACCATGATGCCAGCCAC 300
    QY 301 TACAAGCAGCAGCTGCCCCCAGCCCTCGGAATCTCTGTGCAACCCAGATGATCACTTC 360
    DB 301 TACAAGCAGCAGCTGCCCCCAGCCCTCGGAATCTCTGTGCAACCCAGATGATCACTTC 360
    QY 361 AAAAGTTTCAAAAAGAACTTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAAG 420
    DB 361 GAAAGTTTCAAAAGAACTTGAAGGACTTTCTGTGTTGATCATCCCTTTGACTGTGGAG 420
    QY 421 CCAGCCCAAGATGA 435
    DB 421 CCAGTCCAGGAGTGA 435
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  DEFINITION
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    cDNA clone T9ESTzyj43f02.y1 5' similar to SW:CSF2.HUMAN F04141
    GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
    sequence.
  ACCESSION
    CF341802
  VERSION
    CF341802.1 GI:33831915
  KEYWORDS
    EST.
  SOURCE
    Toxoplasma gondii
  ORGANISM
    Toxoplasma gondii
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Sarcocystidae; Toxoplasma.  
1 (bases 1 to 584)  
Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioke, J.A., White, M.,  
Clifton, S., Pape, D., Martin, J., Wylie, T., Dente, M., Marra, M.,  
Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,  
Ritter, E., Bennett, J., Franklin, C., Tsagaris, W., Ronko, I.,  
Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.  
Toxoplasma EST Project  
Unpublished (2001)  
Contact: Clifton, S.  
Toxoplasma EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: toxo@watson.wustl.edu  
Contact David Sibley (toxost@borcim.wustl.edu) for further  
information relating to organism, libraries, or clone availability.  
Seq primer: -40UP from Gibco.

# FEATURES

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/note="Vector: Modified pBluescript (pBS SK+); Site 1:  
BamHI; Site 2: EcoRI. The cDNA library was constructed by  
Keliang Tang, and Robert Cole at Washington University.  
cDNA was synthesized from poly(A)+ mRNA using the  
template-switching PCR method (SMART cDNA Kit, BD  
Biosciences). First strand cDNA was reverse transcribed  
using the CDS III/3' primer and a 5' template switch  
primer (Smart IV primer). The product of the first strand  
synthesis was PCR amplified using the same primer set and  
the fragments were digested with SfiI. The fragments were  
size selected, ligated into a modified pBluescript vector  
(obtained from Michael White, Montana State University)  
containing directional SfiI sites, and electroporated into  
Electron Blue cells. Vector: SfiI sites were added to  
the multiple cloning region of pBluescript SK+ between the  
BamHI/EcoRI sites. The modified polylinker has the  
following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--  
GGCCGCTCGGCCACGGATCC3' where n=3-4 G nucleotides.  
WARNING: the library contains a small percentage of cDNAs  
derived from the human host cells. Library materials  
provided by David Sibley, Washington University."

# ORIGIN

Query Match 75.7%; Score 329.4; DB 5; Length 584;  
Best Local Similarity 84.8%; Pred. No. 1.8e-82;  
Matches 369; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 1 ATGTGGCTGCAGAACCTGCTTCTTGGGCACCTGTGTTTACAGCATGCCGCCACCCACC 60  
DB 33 ATGTGGCTGCAGAGCTGTGCTTCTTGGGCACCTGTGCTGAGATGAATGCAAGAGCCCGC 92  
QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGATGCCATCAAGAGCCCTGT 120  
DB 93 CCGTCCGACGCCCCAGACACGAGCCCTGGAGCATGTGAATGCCATCCAGAGGCCCGG 152  
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DB 153 CGTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGTAGTGTGCT 212  
QY 181 TGTGAACAGTTTGGACGCCAGAGAGTGCATCGCTGCGAGACTCGGCTGAAGCTGTACAA 240  
DB 213 TCAGAAATGTTTGAAGCTCCAGGAGCCGACCTGCCTACAGACCCGCTGGAGCTGTACAG 272  
QY 241 CAGGGCTTGGGGGGCGCTCATCAAGCTCGAAGGCCCTTCAACCATGATGATGCCAGCCAC 300

Db 273 CAGGGCTTGGGGGGCGCTCATCAAGCTCAAGGCCCTTGAACCATGATGATGCCAGCCAC 332  
QY 301 TACAAGCAGCACTGCCCCCCCACCCTTGAAATCTCTGTGCAACCCAGCATGATCACTTC 360  
DB 333 TACAAGCAGCACTGCCCTCCAAACCCCGAAACTTCTGTGCAACCCAGCATGATCACTTC 392  
QY 361 AAAAGTTTCAAAAAGACCTCAAGGATTTCTGTGTGAGATCCCGTTTGACTGCTGGAG 420  
DB 393 GAAAGTTTCAAAAGAGAACCTGAAGGACTTCTGTCTGTATCCCTTTGACTGCTGGAG 452  
QY 421 CCAGCCCAAGAGTAA 435  
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RESULT 9  
BE873976 895 bp mRNA linear EST 20-OCT-2000  
LOCUS BE873976  
DEFINITION 60148045F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3886571 5',  
mRNA sequence.  
ACCESSION BE873976  
VERSION BE873976.1 GI:10322752  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 895)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/BTP/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E.S. Consortium/LLNL at:  
http://image.llnl.gov  
plate: LLAM9663 row: j column: 12  
High quality sequence stop: 711.  
Location/Qualifiers  
1..895

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/clone\_lib="NIH\_MGC\_69"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."

# ORIGIN

Query Match 75.6%; Score 329; DB 7; Length 895;  
Best Local Similarity 85.0%; Pred. No. 2.6e-82;  
Matches 368; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
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DB 1 GTGGCTGCAGAGCCCTGCTGCTTGGGCACCTGTGCGCATCTCTGCACCCCGCG 60  
QY 63 CCACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGATGCATCAAGAGGCCCTGAG 122  
DB 61 CTCGCCAGCCCGACGACGCGAGCCCTGGAGCATGTGAATGCCATCCAGAGGCCCGCG 120  
QY 123 CTTCTTGAACACAGTAGTAGTGCATGCTGTATCATGAATGAACAGTAGAGTGTGCTTC 182

Db 121 TCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATCTC 180  
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 QY 243 GGGCTTGGGGGCGGACCTCATCAAGCTTGAAGGCGGCTTGAACCATGATGGCCAGCCACTA 302  
 Db 241 GGGCTTGGGGGCGGACCTCACCAGCTCAAGGCGGCTTGAACCATGATGGCCAGCCACTA 300  
 QY 303 CAAGCAGCACTGCCCGCCCGCCCGCTGGAACCTTCTGCTGCAACCCAGATGATCACCTTCAA 362  
 Db 301 CAAGCAGCACTGCCCGCCCGCCCGCTGGAACCTTCTGCTGCAACCCAGATGATCACCTTCAA 360  
 QY 363 AAGTTTCAAAAGAACCTTGAAGGATTTCTGTTTGAAGATCCGTTTGAAGCTGCTGGAAGCC 422  
 Db 361 AAGTTTCAAGGAGCACTTGAAGGACTTCTGCTTGTCTGCTGCTGCTGCTGCTGCTGCTG 420  
 QY 423 AGCCAGCAAGTAA 435  
 Db 421 AGTCCAGGAGTGA 433

RESULT 10  
 CF370833  
 LOCUS  
 DEFINITION  
 TgSTzj59e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii  
 cDNA clone TgSTzj59e12.y1 5' similar to SW:CSF2 HUMAN P04141  
 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR , mRNA  
 sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Toxoplasma gondii  
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 Sarcocystidae; Toxoplasma.  
 1 (bases 1 to 585)  
 Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioke, J.A., White, M.,  
 Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,  
 Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,  
 Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I.,  
 Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.  
 Toxoplasma EST Project  
 Unpublished (2001)  
 Contact: Clifton, S.  
 Toxoplasma EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: toxo@watson.wustl.edu  
 Contact David Sibley (toxostoborcm.wustl.edu) for further  
 information relating to organism, libraries, or clone availability.  
 Seq primer: -40UP from Gibco.  
 Location/Qualifiers  
 1. 585  
 /organism="Toxoplasma gondii"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:5911"  
 /clone="TgSTzj59e12.y1"  
 /dev\_stage="Tachyzoite"  
 /lab\_host="ElectroTen Blue cells (Stratagene)"  
 /clone\_lib="Tg CAST Tachyzoite cDNA Library"  
 /note="Vector: Modified pBluescript (pBS SK+); Site 1:  
 BamHI; Site 2: EcoRI; The cDNA library was constructed by  
 Kellang Tang, and Robert Cole at Washington University.  
 cDNA was synthesized from poly(A)+ mRNA using the  
 template-switching PCR method (SMART cDNA Kit, BD  
 Biosciences). First strand cDNA was reverse transcribed  
 using the CDS III/3' primer and a 5' template switch  
 primer (Smart IV primer). The product of the first strand  
 synthesis was PCR amplified using the same primer set and

FEATURES  
 source

the fragments were digested with SfiI. The fragments were  
 size selected, ligated into a modified pBluescript vector  
 (obtained from Michael White, Montana State University)  
 containing directional SfiI sites, and electroporated into  
 ElectroTen Blue cells. Vector: SfiI sites were added to  
 the multiple cloning region of pBluescript SK+ between the  
 BamHI/EcoRI sites. The modified polylinker has the  
 following sequence: 5'-GAATTCGGCCATTACGCC(G)n-- insert--  
 GGCCGCTCGGCCAGCATCC3' where n=3-4 G nucleotides.  
 WARNING: the library contains a small percentage of cDNAs  
 derived from the human host cells. Library materials  
 provided by David Sibley, Washington University."

## ORIGIN

Query Match 74.3%; Score 323; DB 5; Length 585;  
 Best Local Similarity 83.9%; Pred. No. 1.2e-80;  
 Matches 365; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
 QY 1 ATGTGGCTGCAGAACCTCTCTTCTTGGGCACTGTGTTTACAGATGCCGCCACCCACC 60  
 Db 35 ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGCTGCGCATCTCTGCACCCGCC 94  
 QY 61 CGCCNACCCAGCCCTGTCACTCGGCCCTGGGAGCATGTGGATGCCATCAAGAGGCCCTG 120  
 Db 95 CGCTCGCCCGAGCCCGCAGCAGCGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCG 154  
 QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTAGTCGTC 180  
 Db 155 GTCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATTTAATAGTAGATCATC 214  
 QY 181 TCTGAACGCTTTGACGCGCGAGGAGCTGACATGCTCTGCAGACTGCGCTGAAGCTGTACAA 240  
 Db 215 TCAGAAATGTTTGACCTCCAGAGCGCGACCTGCCTACAGACCCGCTGGAGCTGTACAG 274  
 QY 241 CAGGCTTGGGGGAGGCTCATCAAGCTCGAAGCCCTTGCACCATGATGCCAGCCAC 300  
 Db 275 CAGGCTTGGGGGAGGCTCATCAAGCTCGAAGCCCTTGCACCATGATGCCAGCCAC 334  
 QY 301 TACAAGCAGCAGCTGCCCCCCCCCACTTCTGTGCAACCCAGATGATCACTTTC 360  
 Db 335 TACAAGCAGCAGCTGCCCCCCCCCACTTCTGTGCAACCCAGATGATCACTTTC 394  
 QY 361 AAAAGTTTCAAAAAGAACCTCAAGGATTTCTGTTTGAAGATCCCTTTGACTGCTGGAG 420  
 Db 395 GAAAGTTTCAAAAAGAACCTCAAGGACTTCTGCTTGTCTATCCCCCTTTGACTGCTGGAG 454  
 QY 421 CCAGCCCAAGTAA 435  
 Db 455 CCAGTCCAGGAGTGA 469

RESULT 11  
 CF370966  
 LOCUS  
 DEFINITION  
 TgSTzj59e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii  
 cDNA clone TgSTzj59e12.y1 5' similar to SW:CSF2 HUMAN P04141  
 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR , mRNA  
 sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Toxoplasma gondii  
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 Sarcocystidae; Toxoplasma.  
 1 (bases 1 to 592)  
 Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioke, J.A., White, M.,  
 Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,  
 Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,  
 Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I.,  
 Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.  
 Toxoplasma EST Project  
 Unpublished (2001)

## COMMENT

Contact: Clifton, S.  
Toxoplasma EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: toxo@watson.wustl.edu  
Contact David Sibley (toxoe@borcim.wustl.edu) for further  
information relating to organism, libraries, or clone availability.  
Seq primer: -40UP from Gibco.

## FEATURES

source

1..592  
Location/Qualifiers  
/organism="Toxoplasma gondii"  
/mol\_type="mRNA"  
/db\_xref="taxon:5811"  
/clone="TgESTj58e12.y1"  
/dev\_stage="Tachyzoite"  
/lab\_host="ElectroTen Blue cells (Stratagene)"  
/clone\_lib="Tg CAST Tachyzoite cDNA Library"  
/note="Vector: Modified pBluescript (pBS SK+); Site 1:  
BamHI; Site 2: EcoRI; The cDNA library was constructed by  
Kellang Tang, and Robert Cole at Washington University.  
cDNA was synthesized from poly(A) + mRNA using the  
template-switching PCR method (SMART cDNA Kit, BD  
Biosciences). First strand cDNA was reverse transcribed  
using the CDS III/3' primer and a 5' template switch  
primer (Smart IV primer). The product of the first strand  
synthesis was PCR amplified using the same primer set and  
the fragments were digested with SfiI. The fragments were  
size selected, ligated into a modified pBluescript vector  
(obtained from Michael White, Montana State University)  
containing directional SfiI sites, and electroporated into  
ElectroTen Blue cells. Vector: SfiI sites were added to  
the multiple cloning region of pBluescript SK+ between the  
BamHI/EcoRI sites. The modified polylinker has the  
following sequence: 5'GAATTCGGCATTCAGGCC(G)n-- insert--  
GGCGCCCTCGGCACGATCC3' where n=3-4 G nucleotides.  
WARNING: the library contains a small percentage of cDNAs  
derived from the human host cells. Library materials  
provided by David Sibley, Washington University."

## ORIGIN

Query Match 74.3%; Score 323; DB 5; Length 592;  
Best Local Similarity 83.9%; Pred. No. 1.2e-80;  
Matches 365; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGATCCCGCACCCACC 60  
DB 35 ATGTGGATGCAGAGCTGCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 94  
QY 61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGCCCTG 120  
DB 95 CGCTCGCCAGCCCGCAGCAGCGACCTGGGAGCATGTGAATGCCATCAGGAGGCCCGG 154  
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGATGAACAGTAGTAAGTCGTC 180  
DB 155 CGTCTCTGAACTCGAGTAGAGACACTGCTGCTGAGATGAATGATATAGTAGAATCATC 214  
QY 181 TCTGAAAGCTTTGACGCCGAGAGAGCTGACATGCCCTGCAGACTCGCCTGAAGCTGTACAAA 240  
DB 215 TCAGAAATGTTTGACTCCAGAGCGCGACCTGCCTACAGACCCGCTGGAGCTGTACAG 274  
QY 241 CAGGCTTTCGGGGGAGCCTGTATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300  
DB 275 CAGGCGCTTCGGGGGAGCGCCCAACCAAGCTCAAGGGCCCTTGAACCATGATGCCAGCCAC 334  
QY 301 TACAAGAGCAGCTGCCCGCCCACTTCCCTGTGCAACCCAGATGATCACTTC 360  
DB 335 TACAAGAGCAGCTGCCCTTCACCCCGGAACTTCTGTGCAACCCAGACTATCACTTT 394  
QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTTCTGTGTGAGATCCCGCTTTGACTGTGGAG 420  
DB 395 GAAAGTTTCAAAAGAACTGAAGGACTTCTCTGCTTGTGTCATCCCTTTGACTGTCTGGAG 454

QY 421 CCAGCCCAAGTAA 435  
DB 455 CCAGTCCAGGAGTGA 469

## RESULT 12

BX111836/c

LOCUS

DEFINITION BX111836 NCI\_CGAP Lu5 Homo sapiens cDNA clone IMAGE9998C104061 ;  
IMAGE:1601601, mRNA sequence.

ACCESSION

BX111836

VERSION

BX111836.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 658)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,

Radelof, U., Schneider, B. and Korn, B.

Human Unigeneset - RZPD3

Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGE9998C104061.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-

bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCACAGAAACAGCTATGAC.

Location/Qualifiers

1..658

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE9998C104061 ; IMAGE:1601601"

/tissue\_type="carcinoid"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Lu5"

/note="Organ: lung; Vector: pT7T3D-PacI; 1st strand cDNA

was prepared from neuroendocrine lung carcinoid, and was

then primed with a Not I - oligo(dT) primer.

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library is

normalized. Library was constructed by Bento Soares and M.

Fatima Bonaldo."

## ORIGIN

Query Match 73.3%; Score 319; DB 4; Length 658;  
Best Local Similarity 84.6%; Pred. No. 1.7e-79;  
Matches 358; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
QY 13 AACCTGCTTCTTCTGGGCACTGTGGTTTACAGATGCCGACCCACCCGCCAACCCACG 72  
DB 658 AGCCTGTGCTCTTTGGGCACTGTGGCTTGCAGCATCTCTGCACCCGCCGCTCGCCCCAG 599  
QY 73 CCTGTCACTCGGCCCTGGCAGCATGTGGATGCATCAAGGAGGCCCTGAGCCTTCTGAAC 132  
DB 598 CCGACGCGAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCTCTCTGAAC 539  
QY 133 AACAGTAGTGAACCTGTGCTATCATGAATGAACAGTAGAAGTCGTCTCTGAACGTTT 192



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Db      538 CTGAGTAGAGACACTGCTGCTGAGATGAATGAACACAGTAGAAGTCATCTCAGAAATGTTT 479
QY      193 GACGCCGAGGAGCTGACATGCTCGAGACTCGCCTGAAGCTGTACAAACAGGGCTTGCGG 252
Db      478 GACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAGCTGTACAGCAGGGCTGCGG 419
QY      253 GGCAGCTCATCAAGCTCGAAGGCCCTTGAACATGATGGCCAGGCACATCAAGCAGCAC 312
Db      418 GGCAGCTCACCAGCTCAAGGCTCAAGGGCCCTTGAACATGATGGCCAGGCACATCAAGCAGCAC 359
QY      313 TGCSCCCCCACCTCGAACTTCCTGTGCAACCCAGATGATCACTTCAAAAGTTTCAA 372
Db      358 TGCCTCCAAACCCCGAAATCTTCTGTGCAACCCAGATGATCACTTCAAAAGTTTCAA 299
QY      373 AAGAACTTGAAGGATTTCTGTGTTGAGATCCCGTTTGAAGTGTGGAAGCCAGCCAGAG 432
Db      298 GAGACCTGAAGGACTTCTGCTGTGATCCCTTGAAGTGTGGAAGCCAGTCCAGGAG 239
QY      433 TAA 435
Db      238 TGA 236

RESULT 13
LOCUS   CB457551
DEFINITION 714908 MARC 6BOV Bos taurus cDNA 5', mRNA linear EST 26-MAR-2003
ACCESSION CB457551
VERSION   CB457551.1 GI:29263933
KEYWORDS EST.
SOURCE   Bos taurus (cattle)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 561)
AUTHORS Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
          Wray,J.E. and Keagle,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called with phred v0.020425.c and
          trimmed with the aid of the trim_alt option. Vector identified with
          cross_match v0.990329.
          Plate: FQ8072 row: H column: 12
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          Location/Qualifiers
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     /lab_host="DH10B"
     /clone_lib="MARC 6BOV"
     /note="Vector: pDON3.1; Site 1: EcoRI; Site 2: NotI;
     Library made with RNA pooled from multiple tissues
     including liver, lung, hypothalamus, pituitary, and
     placenta/endometrium."

ORIGIN
Query Match 73.1%; Score 318.2; DB 4; Length 561;
Best Local Similarity 84.8%; Pred. No. 2.7e-79;
Matches 369; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY      1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGGTTTACAGCATGCCGCGACCCACC 60
Db      17 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGGTTTCTGAGCTTCTCGCACCTACT 76

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QY      61 GCGCAACCCAGCCCTGTCTCACTCGGCCCTTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 120
Db      77 GCGCCACCCCAACACTGCCACCGGCCCTTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 136
QY      121 AGCCTTCTGACCAACAGTAGTACACTGCTGCTATCATGAATGAACACAGTAGAAGTCGTC 180
Db      137 AGCCTTCTGAAACACAGCAGTGACACTGATGCTGTGTGAATGACAC---AGAAGTCGTC 193
QY      181 TCTGAAAGCTTTGACGCGGAGGAGCTGACATCGCTGCAGACTCGCTGAAGCTGTACAAA 240
Db      194 TCTGAAAGCTTTGACTCCAGGAACCAACGCTGCTGCAGACTCGCTGAAGCTGTACAA 253
QY      241 CAGGCTTGCGGGGCAGCTCATCAAGCTCGAAGCCCTTGAACCATGATGCCAGCCAC 300
Db      254 AACGCTTGCAGGGCAGCTCACTAGTCTCATGCGGCTCTTGACCATGATGCCAGCCAC 313
QY      301 TACAGCAGCACTGCCCCCACCCTCGAAGTCTGCAAACTTCTGTGCAACCCAGATGATCACTTC 360
Db      314 TACGAGAAACACTGCCCCACCACCCCGGAACTTCTCTGTGGAACCCAGTTTATCAGCTTC 373
QY      361 AAAAGCTTTCAAAAAGAACTGAAGGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
Db      374 AAAAATTTCAAAGAGGACTGAGGAGTTCTTTTATCATTTCCCTTTGACTGCTGGGA 433
QY      421 CCAGCCCAAGATGA 435
Db      434 CCAGCCCAAGATGA 448

RESULT 14
LOCUS   BM539160
DEFINITION hb05e10.g1 Canis cDNAs from testes cells Canis familiaris cDNA
ACCESSION BM539160
VERSION   BM539160.1 GI:18820855
KEYWORDS EST.
SOURCE   Canis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
          Canis.
REFERENCE 1 (bases 1 to 572)
AUTHORS O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V.,
          Cunniss,D., Dedhia,N.N., de la Bastide,M., Katzenberger,F.,
          King,L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U.,
          Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T.,
          Preston,R. and Hannon,G.J.
          Expressed sequence tags from Canis familiaris (dog) (2002)
          Unpublished (2002)
          Contact: W. Richard McCombie
          Lita Annenberg Hazen Genome Sequencing Center
          Cold Spring Harbor Laboratory
          PO Box 100, Cold Spring Harbor, NY 11724, USA
          Tel: 516 367 8884
          Fax: 516 367 8874
          Email: mcombie@cshl.org
          Plate: hb05 row: e column: 10
          Seq primer: -21M13UnivRev
          High quality sequence stop: 572.
          Location/Qualifiers
FEATURES             source
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     /note="Vector: Lambda Zap II; The library was produced by
     Greg Hannon and Raymond Preston (Cold Spring Harbor
     Laboratory). This library is oligo(dT) primed using
     stratagene zap cDNA synthesis kit. It was made from dog
     testes. Please contact Greg Hannon (hannon@cshl.org) with

```

any library related inquiries."

ORIGIN

Query Match 73.1%; Score 318.2; DB 2; Length 572;  
Best Local Similarity 83.2%; Pred. No. 2.8e-79;  
Matches 362; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1 ATGTGGCTGCGAAGACCTGCTTCTTCTGGGCACTGTGGTTTACAGGATCCCGCAGCCACC 60  
Db 29 ATGTGGCTGCGAAGACCTGCTTCTTCTGGGCACTGTGGTTTACAGGATCCCGCAGCCACC 88

Qy 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 120  
Db 89 CGCTCACCACCCCTTGTCACTCGGCCCTTCTCAGCAGTGGATGCCATCCAGGAGCCCTG 148

Qy 121 AGCCCTTCTGAACAAACAGTAGTGACATGCTGCTATCATGAATGAACAGTAGTAAGTGCCT 180  
Db 149 AGCCCTTCTGAACAAACAGTAGTGACATGCTGCTGATGAATAAAGCAGTAGTAAGTGCCT 208

Qy 181 TCTGAAAGCTTTGACCGCGAGAGCTGACATGCTCGAGACTCGGCTGAAGCTGTACAAA 240  
Db 209 TCTGAAAGCTTTGACCGCGAGAGCTGACATGCTCGAGACTCGGCTGAAGCTGTACAAA 268

Qy 241 CAGGCTTTGCGGGGCGAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300  
Db 269 GAGGCTTTGCGGGGCGAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 328

Qy 301 TACAGCAGCAGCTGCCCCCCCCCAGGAACTTCTGTGCAACCCAGATGATCACTTC 360  
Db 329 TATAAGCAGCAGCTGCCCCCCCCCAGGAACTTCTGTGCAACCCAGATGATCACTTC 388

Qy 361 AAAAGTTTCAAAAGAACTGAAGATTTCTGTGTGAGATCCCGTTTGAAGCTGTGGAAG 420  
Db 389 AAAAGTTTCAAAAGAACTGAAGATTTCTGTGTGAGATCCCGTTTGAAGCTGTGGAAG 448

Qy 421 CCAGCCCAAGATGA 435  
Db 449 CCAGTCAAGAAGTGA 463

RESULT 15  
CF614774

LOCUS CES009198 Bos taurus muscle cDNA library Bos taurus cDNA clone  
DEFINITION CCL009198 5', mRNA sequence.

ACCESSION CF614774  
VERSION CF614774.1 GI:37240821  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus

REFERENCE Wang,Y.H., Byrne,K.A., Reverter,A., Harper,G.S., Taniguchi,M.,  
AUTHORS McWilliam,S.M., Mannen,H., Oyama,K. and Lehnert,S.A.  
TITLE Transcriptional profiling of skeletal muscle tissue from two breeds  
of cattle

JOURNAL Mamm. Genome 16 (3), 201-210 (2005)  
PUBMED 15834637  
COMMENT Contact: Dr Sigrid Lehnert  
Functional Genomics Lab  
CSIRO Livestock Industries  
Level 5, Queensland Bioscience Precinct, University of Queensland,  
306 Carmody Road St.Lucia QLD Australia  
Tel: 07 3214 2445  
Fax: 07 3214 2480  
Email: Sigrid.Lehnert@csiro.au  
Plate: 08 row: D column: 01.  
Location/Qualifiers  
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/organism="Bos taurus"  
/mol\_type="mRNA"

FEATURES  
source

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/clone\_lib="Bos taurus muscle cDNA library"  
/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site\_1:  
EcoRI; Site\_2: Xho I; Library made from skeletal muscle of  
a 14 month old Angus steer."

ORIGIN

Query Match 72.5%; Score 315.2; DB 5; Length 672;  
Best Local Similarity 84.1%; Pred. No. 2.1e-78;  
Matches 366; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

Qy 1 ATGTGGCTGCGAAGACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCGACCCACC 60  
Db 19 ATGTGGNNAGAACCTGCTTCTCTGGGCACTGTGGTTCTGCAGCTTCTCGCACCTACT 78

Qy 61 CGCCAAACCCAGCCCTGTCACCTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 120  
Db 79 CGCCAAACCCAGCTGCCACCCGCGCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 138

Qy 121 AGCCTTCTGAACCAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTAAGTGCCT 180  
Db 139 AGCCTTCTGAACCAACAGTAGTGACACTGCTGCTGATGAATGACAC---AGAACTCGTC 195

Qy 181 TCTGAAAGCTTTGACCGCGAGGAGCTGACATGCTCGCTGCAGACTCGCCTGAAGCTGTACAAA 240  
Db 196 TCTGAAAGCTTTGACTCCAGGACCAACGTCGCTGCAGACTCGCCTGAAGCTGTACAA 255

Qy 241 CAGGCTTTGCGGGGCGAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300  
Db 256 AACGGCTTGACGGGCGAGCTCACTAGTCTCATGGGCTCTTGCACCATGATGCCAGCCAC 315

Qy 301 TACAGCAGCAGCTGCCCCCCCCCAGGAACTTCTGTGTGAGATCCCGTTTGAAGCTGTGGAAG 360  
Db 316 TACGAGAAACACTGCCACCCACCCCGGAACTTCTCTGTGGAACCCAGTTTATCAGCTTC 375

Qy 361 AAAAGTTTCAAAAGAACTGAAGATTTTCTGTGTGAGATCCCGTTTGAAGCTGTGGAAG 420  
Db 376 AAAAGTTTCAAGAGGAGCTGAGGAGTTCTTTTATCATTCCTCTTGAAGCTGTGGAAG 435

Qy 421 CCAGCCCAAGATGA 435  
Db 436 CCAGCCCAAGATGA 450

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Job time : 3398 secs



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 01:01:29 ; Search time 164 Seconds  
(without alignments)  
4963.002 Million cell updates/sec

Title: US-10-614-481-8  
Perfect score: 435  
Sequence: 1 atgtggctgcagaacctgct.....ggaagccagccagaaagtaa 435

Scoring table: IDENTITY NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq: \*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq: \*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq: \*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq: \*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq: \*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq: \*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq: \*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq: \*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq: \*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	3	US-09-589-460-8
2	332.6	76.5	444	3	Sequence 119, App Sequence 119, App
3	332.6	76.5	444	3	Sequence 121, App Sequence 121, App
4	332.6	76.5	444	3	Sequence 119, App Sequence 119, App
5	332.6	76.5	444	3	Sequence 121, App Sequence 121, App
6	332.6	76.5	444	5	Sequence 119, App Sequence 119, App
7	332.6	76.5	444	5	Sequence 121, App Sequence 121, App
8	332.6	76.5	798	2	Sequence 10, App Sequence 10, App
9	332.6	76.5	798	2	Sequence 10, App Sequence 10, App
10	332.6	76.5	798	2	Sequence 10, App Sequence 10, App
11	331.2	76.1	432	3	Sequence 9, App Sequence 9, App
12	331.2	76.1	432	3	Sequence 8, App Sequence 8, App
13	331	76.1	435	3	Sequence 8, App Sequence 8, App
14	331	76.1	435	3	Sequence 8, App Sequence 8, App
15	331	76.1	789	5	Sequence 2706, App Sequence 2706, App
16	331	76.1	5115	5	Sequence 2709, App Sequence 2709, App
17	329.6	75.8	432	3	Sequence 122, App Sequence 122, App
18	329.6	75.8	432	3	Sequence 123, App Sequence 123, App
19	329.6	75.8	432	3	Sequence 122, App Sequence 122, App
20	329.6	75.8	432	3	Sequence 123, App Sequence 123, App
21	329.6	75.8	432	3	Sequence 7, App Sequence 7, App
22	329.6	75.8	432	3	Sequence 7, App Sequence 7, App
23	329.6	75.8	432	5	Sequence 122, App Sequence 122, App

C	24	329.6	75.8	432	5	US-10-262-439-123	Sequence 123, App
	25	329.6	75.8	1032	3	US-09-555-165-8	Sequence 8, Appl
	26	329.6	75.8	1032	3	US-09-555-165-10	Sequence 10, Appl
	27	329.4	75.7	435	3	US-10-188-056-32	Sequence 32, Appl
	28	329.4	75.7	496	2	US-08-184-009-191	Sequence 191, App
	29	329.4	75.7	496	2	US-08-458-356-191	Sequence 191, App
	30	329.4	75.7	496	3	US-08-460-736-191	Sequence 191, App
	31	329.4	75.7	496	3	US-09-535-370-191	Sequence 191, App
	32	329.4	75.7	496	3	US-09-663-667-191	Sequence 191, App
	33	329.4	75.7	756	3	US-09-016-434-1195	Sequence 1195, Ap
	34	329.4	75.7	1318	3	US-09-310-842-3	Sequence 3, Appli
	35	328	75.4	945	2	US-08-750-128-7	Sequence 7, Appli
	36	327.8	75.4	435	3	US-10-188-056-34	Sequence 34, Appl
	37	326.4	75.0	969	2	US-08-750-128-4	Sequence 4, Appli
	38	318.2	73.1	809	2	US-08-259-696B-6	Sequence 6, Appli
	39	318.2	73.1	809	2	US-08-259-696B-8	Sequence 8, Appli
	40	318.2	73.1	809	2	US-08-902-513-6	Sequence 6, Appli
	41	318.2	73.1	809	2	US-08-902-513-8	Sequence 8, Appli
	42	315	72.4	1011	3	US-09-976-594-275	Sequence 275, App
	43	301.6	69.3	660	10	5391485-2	Patent No. 5391485
	44	301.6	69.3	661	10	5229496-1	Patent No. 5229496
	45	296.4	68.1	1588	2	US-09-146-283-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-589-460-8  
; Sequence 8, Application US/09589460  
; Patent No. 6645740  
; GENERAL INFORMATION:  
; APPLICANT: Bublout, et al.  
; TITLE OF INVENTION: Equine GM-CSF  
; FILE REFERENCE: 454313-2334.1  
; CURRENT APPLICATION NUMBER: US/09/589,460  
; CURRENT FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: 60/138,843  
; PRIOR FILING DATE: 1999-06-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 435  
; TYPE: DNA  
; ORGANISM: Equine sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(432)  
; OTHER INFORMATION: coding sequence of equine GM-CSF gene  
US-09-589-460-8

Query Match	100.0%	Score 435;	DB 3;	Length 435;
Best Local Similarity	100.0%	Pred. No. 5.2e-118;	Indels 0;	Gaps 0;
Matches 435;	Conservative 0;	Mismatches 0;		
QY	1	ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGTGGTTTACAGCATGCCCGACCCACC	60	
Db	1	ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGTGGTTTACAGCATGCCCGACCCACC	60	
QY	61	CGCCCAACCCAGCCCTGTCTACTGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120	
Db	61	CGCCCAACCCAGCCCTGTCTACTGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120	
QY	121	AGCCTTCTGAAACAAACAGTAGTAGTGCATGCTGTATCATGAATGAAACAGTAGAAGTCGTC	180	
Db	121	AGCCTTCTGAAACAAACAGTAGTAGTGCATGCTGTATCATGAATGAAACAGTAGAAGTCGTC	180	
QY	181	TCTGAAACCTTTTGACGCCGAGGAGCTGCATGCCTGCAGACTCGCCTGAAGCTGTACAA	240	
Db	181	TCTGAAACCTTTTGACGCCGAGGAGCTGCATGCCTGCAGACTCGCCTGAAGCTGTACAA	240	
QY	241	CAGGGCTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC	300	

Db 241 CAGGGCTTGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
QY 301 TACAAGCAGACTGCCCCCCCCCACTTCTGTGGAACCCAGATGATCACTTC 360  
Db 301 TACAAGCAGACTGCCCCCCCCCACTTCTGTGGAACCCAGATGATCACTTC 360  
QY 361 AAAAGTTTCAAAAAGAACTGAAGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420  
Db 361 AAAAGTTTCAAAAAGAACTGAAGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420  
QY 421 CCAGCCCAAGATAA 435  
Db 421 CCAGCCCAAGATAA 435

RESULT 2  
US-09-322-409-119  
; Sequence 119, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 119  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Felis catus  
; NAME/KEY: CDS  
; LOCATION: (10)..(441)  
US-09-322-409-119

Query Match 76.5%; Score 332.6; DB 3; Length 444;  
Best Local Similarity 85.3%; Pred. No. 6.9e-88;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGTTTACAGCATGCCGACCCACC 60  
Db 10 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGTTTACAGCATGCCGACCCACC 69  
QY 61 CGCCAAACCCAGCCCTGTCTCGGCCCTGGAGCATGTGGATGCCATCAAGAGGCCCTG 120  
Db 70 AGTTCAACCCAGCTGTCTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGGCCCTG 129  
QY 121 AGCCCTTCTGAACAACAGTAGTGACCTGCTGTATCATGAATGAACAGTAGAGTCGTC 180  
Db 130 AGCCCTTCTGAACAACAGTAGTGAAATACTGCTGTGATGAATGAACAGTAGAGTCGTC 189  
QY 181 TCTGAAACGTTTGAAGCCCGAGGAGTGACATGCCTGCAGACTCGCTGAAGCTGTACAA 240  
Db 190 TCTGAAATGTTTGACCTCGAGGCGGAAATGCCTGCAGACTCACCTAAAGCTGTACGAG 249  
QY 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
Db 250 CAGGGCTTACGGGGAGCCCTCATCAAGCTCAAGGAGCCCTCTGAGAATGATGCCAACCAT 309  
QY 301 TACAAGCAGACTGCCCCCCCCCACTTCTGTGGAACCCAGATGATCACTTC 360  
Db 310 TACAAGCAGACTGCCCCCCCCCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 369  
QY 361 AAAAGTTTCAAAAAGAACTGAAGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420  
Db 370 AAAAATTTCAAAAGAGAACTCTGAAGGATTTTCTGTTTAAACAACCCCTTTGACTGCTGGGA 429

QY 421 CCAGCCCAAGATAA 435  
Db 430 CCAGCCCAAGATAA 444

RESULT 3  
US-09-322-409-121/C  
; Sequence 121, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 121  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Felis catus  
US-09-322-409-121

Query Match 76.5%; Score 332.6; DB 3; Length 444;  
Best Local Similarity 85.3%; Pred. No. 6.9e-88;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGTTTACAGCATGCCGACCCACC 60  
Db 435 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGTTTACAGCATCTCTGCACCCACC 376  
QY 61 CGCCAAACCCAGCCCTGTCTCGGCCCTGGAGCATGTGGATGCCATCAAGAGGCCCTG 120  
Db 375 AGTTCAACCCAGCTGTCTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGGCCCTG 316  
QY 121 AGCCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180  
Db 315 AGCCCTTCTGAACAACAGTAGTGAAATACTGCTGTGATGAATGAACAGTAGAGTCGTC 256  
QY 181 TCTGAAACGTTTGAAGCCCGAGGAGTGACATGCCTGCAGACTCGCTGAAGCTGTACAAA 240  
Db 255 TCTGAAATGTTTGAACCTGAGGAGCCGAAATGCCTGCAGACTCACCTAAAGCTGTACGAG 196  
QY 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
Db 195 CAGGGCTTACGGGGAGCCCTCATCAAGCTCAAGGAGCCCTCTGAGAATGATGCCAACCAT 136  
QY 301 TACAAGCAGACTGCCCCCCCCCACTTCTGTGGAACCCAGATGATCACTTC 360  
Db 135 TACAAGCAGACTGCCCCCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 76  
QY 361 AAAAGTTTCAAAAAGAACTGAAGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420  
Db 75 AAAAATTTCAAAAGAGAACTCTGAAGGATTTTCTGTTTAAACAACCCCTTTGACTGCTGGGA 16  
QY 421 CCAGCCCAAGATAA 435  
Db 15 CCAGCCCAAGATAA 1

RESULT 4  
US-09-451-527-119  
; Sequence 119, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee

APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 1999-12-01  
EARLIER FILING DATE: 1999-05-28  
EARLIER FILING DATE: 1999-05-28  
EARLIER FILING DATE: 1999-05-28  
EARLIER FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 119  
LENGTH: 444  
TYPE: DNA  
ORGANISM: Felis catus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (10)..(441)  
US-09-451-527-119

Query Match 76.5%; Score 332.6; DB 3; Length 444;  
Best Local Similarity 85.3%; Pred. No. 6.9e-88;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCGCCACCCACC 60  
DB 10 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCGCCACCC 69  
QY 61 CGCCCAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
DB 70 AGTTCAACCCAGCTCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 129  
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGTCTGTATCATGAAATGAACAGTAGAAGTCGTC 180  
DB 130 AGCCTTCTGAACAACAGTAGTGAAATAACTGTGTGATGAATGAAGCAGTAGAAGTCGTC 189  
QY 181 TCTGAAAGCTTTGACCGCGAGGAGCTGACATCCCTGCAGACTCGCTGAAGCTGTACAAA 240  
DB 190 TCTGAAATGTTTGACCTGAGGAGCGGAATGCCCTGCAGACTCACCTAAGCTGTACGAG 249  
QY 241 CAGGCTTTCGCGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGAACCATGTATGCCAGCCAC 300  
DB 250 CAGGCTTTCGCGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGAACCATGTATGCCAGCCAC 309  
QY 301 TACAAGCAGCACTGCCCGCCACCCCTGGAACCTTCTGTGTGCAACCCAGATGATCACTTTC 360  
DB 310 TACAAGCAGCACTGCCCGCCCTTACTCCGGAACCGCCCTGTGAAACCCAGACTATCACTTTC 369  
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTGACTGCTGGAAG 420  
DB 370 AAAAATTTCAAGAAGAACTGAAGGATTTTCTGTTTAAACCCCTTTGACTGCTGGGA 429  
QY 421 CCAGCCCAAGAGTAA 435  
DB 430 CCAGACCAGAGTAA 444

RESULT 5  
US-09-451-527-121/c  
Sequence 121, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: US/09/451,527  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
CURRENT APPLICATION NUMBER: US/09/451,527

CURRENT FILING DATE: 1999-12-01  
EARLIER FILING DATE: 09/322,409  
EARLIER FILING DATE: 1999-05-28  
EARLIER FILING DATE: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 121  
LENGTH: 444  
TYPE: DNA  
ORGANISM: Felis catus  
US-09-451-527-121

Query Match 76.5%; Score 332.6; DB 3; Length 444;  
Best Local Similarity 85.3%; Pred. No. 6.9e-88;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCGCCACCCACC 60  
DB 435 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCGCCACCC 376  
QY 61 CGCCCAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
DB 375 AGTTCAACCCAGCTCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 316  
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGTCTGTATCATGAAATGAACAGTAGAAGTCGTC 180  
DB 315 AGCCTTCTGAACAACAGTAGTGAAATAACTGTGTGATGAATGAAGCAGTAGAAGTCGTC 256  
QY 181 TCTGAAAGCTTTGACCGCGAGGAGCTGACATCCCTGCAGACTCGCTGAAGCTGTACAAA 240  
DB 255 TCTGAAATGTTTGACCTGAGGAGCGGAATGCCCTGCAGACTCACCTAAGCTGTACGAG 196  
QY 241 CAGGCTTTCGCGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGAACCATGTATGCCAGCCAC 300  
DB 195 CAGGCTTTCGCGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGAACCATGTATGCCAGCCAC 136  
QY 301 TACAAGCAGCACTGCCCGCCACCCCTGGAACCTTCTGTGTGCAACCCAGATGATCACTTTC 360  
DB 135 TACAAGCAGCACTGCCCGCCCTTACTCCGGAACCGCCCTGTGAAACCCAGACTATCACTTTC 76  
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTGACTGCTGGAAG 420  
DB 75 AAAAATTTCAAGAAGAACTGAAGGATTTTCTGTTTAAACCCCTTTGACTGCTGGGA 16  
QY 421 CCAGCCCAAGAGTAA 435  
DB 15 CCAGACCAGAGTAA 1

RESULT 6  
US-10-262-439-119  
Sequence 119, Application US/10262439  
Patent No. 7026139  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-kee  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/10/262,439  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: US/09/451,527  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 119

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; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(441)
US-10-262-439-119

Query Match      76.5%; Score 332.6; DB 5; Length 444;
Best Local Similarity 85.3%; Pred. No. 6.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
   |||||
Db 10 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATCTCTGCACCCACC 69
   |||||

QY 61 CGCCCAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
   |||||
Db 70 AGTTACCCAGCTGTCTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGGCCCTG 129
   |||||

QY 121 AGCCTTCTGAACAAACAGTAGTGACACTGTGCTATCATGAATGAAGAAACAGTAGTAAGTCGTC 180
   |||||
Db 130 AGCCTTCTGAACAAACAGTAGTGAATAAATGCTGTGATGAATGAAGCAAGTAGTAAGTCGTC 189
   |||||

QY 181 TCTGAAAGCTTTGACCGCGAGGAGCTGACATCGCTGCAAGCTCGCTGCAAGCTGACAAA 240
   |||||
Db 190 TCTGAAATGTTTGACCCCTGAGGAGCGGAATGCCCTGCAGACTCACCTAAAGCTGTACGAG 249
   |||||

QY 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
   |||||
Db 250 CAGGGCTTACGGGAGCCCTCATCAAGCTCGAAGGCCCTTGAGATGATGCCAACCAT 309
   |||||

QY 301 TACAAGCAGCACTGCCCCCCTTACTCGGAAACGCTTGTGCAACCCAGATATCACCTTC 360
   |||||
Db 310 TACAAGCAGCACTGCCCCCCTTACTCGGAAACGCTTGTGCAACCCAGATATCACCTTC 369
   |||||

QY 361 AAAAGTTTCAAAAGAACTGGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGGAG 420
   |||||
Db 370 AAAAATTTCAAAGAGAATCTGAAGGATTTCTGTTTAAACACCCCTTTGACTGCTGGGGA 429
   |||||

QY 421 CCAGGCCAGAGTAA 435
   |||||
Db 430 CCAGACCAGAGTAA 444
   |||||

RESULT 7
US-10-262-439-121/c
; Sequence 121, Application US/10262439
; Patent No. 7026139
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Keo
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus
US-10-262-439-121
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Query Match      76.5%; Score 332.6; DB 5; Length 444;
Best Local Similarity 85.3%; Pred. No. 6.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
   |||||
Db 435 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATCTCTGCACCCACC 376
   |||||

QY 61 CGCCCAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
   |||||
Db 375 AGTTACCCAGCTGTCTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGGCCCTG 316
   |||||

QY 121 AGCCTTCTGAACAAACAGTAGTGACACTGTGCTATCATGAATGAAGAAACAGTAGTAAGTCGTC 180
   |||||
Db 315 AGCCTTCTGAACAAACAGTAGTGAATAAATGCTGTGATGAATGAAGCAAGTAGTAAGTCGTC 256
   |||||

QY 181 TCTGAAAGCTTTGACCGCGAGGAGCTGACATCGCTGCAAGCTCGCTTGAAGCTGTACAAA 240
   |||||
Db 255 TCTGAAATGTTTGACCCCTGAGGAGCGGAATGCCCTGCAGACTCACCTAAAGCTGTACGAG 196
   |||||

QY 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
   |||||
Db 195 CAGGGCTTACGGGAGCCCTCATCAGCCTCAAGGAGCCCTTGAGAAATGATGCCAACCAT 136
   |||||

QY 301 TACAAGCAGCACTGCCCCCCTTACTCGGAAACGCTTGTGCAACCCAGATATCACCTTC 360
   |||||
Db 135 TACAAGCAGCACTGCCCCCCTTACTCGGAAACGCTTGTGCAACCCAGATATCACCTTC 76
   |||||

QY 361 AAAAGTTTCAAAAGAACTGGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGGAG 420
   |||||
Db 75 AAAAATTTCAAAGAGAATCTGAAGGATTTCTGTTTAAACACCCCTTTGACTGCTGGGGA 16
   |||||

QY 421 CCAGGCCAGAGTAA 435
   |||||
Db 15 CCAGACCAGAGTAA 1
   |||||

RESULT 8
US-08-133-979A-10
; Sequence 10, Application US/08133979A
; Patent No. 5589582
; GENERAL INFORMATION:
; APPLICANT: Hawley, Robert J.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Rosa, Margaret D.
; APPLICANT: Monroy, Rodney L.
; APPLICANT: Schacter, Bernice Z.
; TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines Therei
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,979A
; FILING DATE: October 8, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Herron, Charles J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 61750-79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 798 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: DOUBLE  
TOPOLOGY: LINEAR  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-133-979A-10

Query Match 76.5%; Score 332.6; DB 2; Length 798;  
Best Local Similarity 85.3%; Pred. No. 8.9e-88;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACC 60  
DB |||||  
QY 30 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACC 89  
DB |||||  
QY 61 CGCCCAACCCAGCCCTGTCTACTGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 120  
DB |||||  
QY 90 CGCCCAACCCAGCCCTGTCTACTGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 149  
DB |||||  
QY 121 AGCCTTCTGAACAAACAGTAGTACACTGCTGTATCATGATGAATGAACAGTAGAGTCGTC 180  
DB |||||  
QY 150 AGCCTTCTGAACAAACAGTAGTACACTGCTGTATCATGATGAATGAACAGTAGAGTCGTC 209  
DB |||||  
QY 181 TCTGAAACCTTTACAGCCGAGGAGGTGACATGCTGCAGACTCGGCTGAAGCTGTACAAA 240  
DB |||||  
QY 210 TGTGAATGTTTGACCCCAAGAGCGCATGGTGCAGACTCGCTGAACCTGTACAA 269  
DB |||||  
QY 241 CAGGCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGAACATGATGCCAGCCAC 300  
DB |||||  
QY 270 CAGGCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGAACATGATGCCAGCCAC 329  
DB |||||  
QY 301 TACAAGCAGCACTGCCCCCCTCAAGCTCGAAGGCCCTTGAACATGATGCCAGCCAC 360  
DB |||||  
QY 330 TATGAGCAGCACTGCCCCCCTCAAGCTCGAAGGCCCTTGAACATGATGCCAGCCAC 389  
DB |||||  
QY 361 AAAAGTTTCAAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGAG 420  
DB |||||  
QY 390 AAAAGTTTCAAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGAG 449  
DB |||||

## RESULT 9

US-08-436-890-10  
Sequence 10, Application US/08436890  
Patent No. 5858963

## GENERAL INFORMATION:

APPLICANT: Hawley, Robert J.  
APPLICANT: Ponath, Paul D.  
APPLICANT: Rosa, Margaret D.  
APPLICANT: Monroy, Rodney L.  
APPLICANT: Schacter, Bernice Z.

TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines There

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: MS-DOS 6.0

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,890

FILING DATE: May 8, 1995

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Herron, Charles J.  
REGISTRATION NUMBER: 28,019  
REFERENCE/DOCKET NUMBER: 61750-139  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 798 BASE PAIRS

TYPE: NUCLEIC ACID

STRANDEDNESS: DOUBLE

TOPOLOGY: LINEAR

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-436-890-10

Query Match 76.5%; Score 332.6; DB 2; Length 798;  
Best Local Similarity 85.3%; Pred. No. 8.9e-88;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACC 60  
DB |||||  
QY 30 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACC 89  
DB |||||  
QY 61 CGCCCAACCCAGCCCTGTCTACTGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 120  
DB |||||  
QY 90 CGCCCAACCCAGCCCTGTCTACTGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 149  
DB |||||  
QY 121 AGCCTTCTGAACAAACAGTAGTACACTGCTGTATCATGATGAATGAACAGTAGAGTCGTC 180  
DB |||||  
QY 150 AGCCTTCTGAACAAACAGTAGTACACTGCTGTATCATGATGAATGAACAGTAGAGTCGTC 209  
DB |||||  
QY 181 TCTGAAACCTTTACAGCCGAGGAGGTGACATGCTGCAGACTCGGCTGAAGCTGTACAAA 240  
DB |||||  
QY 210 TGTGAATGTTTGACCCCAAGAGCGCATGGTGCAGACTCGCTGAACCTGTACAA 269  
DB |||||  
QY 241 CAGGCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGAACATGATGCCAGCCAC 300  
DB |||||  
QY 270 CAGGCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGAACATGATGCCAGCCAC 329  
DB |||||  
QY 301 TACAAGCAGCACTGCCCCCCTCAAGCTCGAAGGCCCTTGAACATGATGCCAGCCAC 360  
DB |||||  
QY 330 TATGAGCAGCACTGCCCCCCTCAAGCTCGAAGGCCCTTGAACATGATGCCAGCCAC 389  
DB |||||  
QY 361 AAAAGTTTCAAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGAG 420  
DB |||||  
QY 390 AAAAGTTTCAAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGAG 449  
DB |||||

## RESULT 10

US-08-451-213-10

Sequence 10, Application US/08451213

Patent No. 5863528

GENERAL INFORMATION:

APPLICANT: Hawley, Robert J.

APPLICANT: Ponath, Paul D.

APPLICANT: Rosa, Margaret D.

APPLICANT: Monroy, Rodney L.

APPLICANT: Schacter, Bernice Z.

TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines There

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA

;; ZIP: 07068  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch diskette  
;; COMPUTER: IBM PC Compatible  
;; OPERATING SYSTEM: MS-DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/451,213  
;; FILING DATE: 26-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/133,979  
;; FILING DATE: October 8, 1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Herron, Charles J.  
;; REGISTRATION NUMBER: 28,019  
;; REFERENCE/DOCKET NUMBER: 61750-79  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-994-1700  
;; TELEFAX: 201-994-1744  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 798 BASE PAIRS  
;; TYPE: NUCLEIC ACID  
;; STRANDEDNESS: DOUBLE  
;; TOPOLOGY: LINEAR  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
US-08-451-213-10

Query Match 76.5%; Score 332.6; DB 2; Length 798;  
Best Local Similarity 85.3%; Pred. No. 8.9e-88;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
  
QY 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 60  
DB |||||  
QY 30 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCCGTCCCACC 89  
DB |||||  
QY 61 CGCCAAACCAGCCCTGTCTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 120  
DB |||||  
QY 90 CGCCCAACCAGCCCTGTCTACCGGGCCCTGGCAGCATGTGGATGCCATCAAGAAGCCCTG 149  
DB |||||  
QY 121 AGCCTTCTGAACACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180  
DB |||||  
QY 150 AGCCTTCTAAACACAGTAGTGACACAGCGGCTGTGATGAATGAACAGTAGAGTCGTC 209  
DB |||||  
QY 181 TCTGAAACCTTTGAGCCGCGAGGAGCTGACATGCCTGCAGACTCGCTGAAAGCTGTACAA 240  
DB |||||  
QY 210 TGTGAATGTTTGACCCCGCAGGCGGACATGGGTGCAGACTCGCTGAACTGTACAG 269  
DB |||||  
QY 241 CAGGGCTTGGGGGCGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCAC 300  
DB |||||  
QY 270 CAGGGCTTGGGGGCGAGCCCTCATAGGCTCAAGAGCCCTTGACTCTGTTGGCCAAAGCAC 329  
DB |||||  
QY 301 TACAAGCAGCACTGCCCCCGCCCTTCTGTGCAACCCAGATGATCACTTC 360  
DB |||||  
QY 330 TATGAGCAGCACTGCCCCCTCAGGAGAACTTCTGTGAAACCCAGTCTATCACTTC 389  
DB |||||  
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420  
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QY 421 CCAGGCCAGAAGTAA 435  
DB |||||  
QY 450 CCAGTCAAAAAGTAA 464  
DB |||||

RESULT 11  
US-09-617-594A-9  
; Sequence 9, Application US/09617594A  
; Patent No. 6541458  
; GENERAL INFORMATION:  
; APPLICANT: Audonnet, et al.

;; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V  
;; FILE REFERENCE: 454313-3151.1  
;; CURRENT APPLICATION NUMBER: US/09/617,594A  
;; CURRENT FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/193,332  
;; PRIOR FILING DATE: 2000-03-30  
;; PRIOR APPLICATION NUMBER: France 00 01761  
;; PRIOR FILING DATE: 2000-02-11  
;; PRIOR APPLICATION NUMBER: France 99 09421  
;; PRIOR FILING DATE: 1999-07-16  
;; NUMBER OF SEQ ID NOS: 26  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 9  
;; LENGTH: 432  
;; TYPE: DNA  
;; ORGANISM: Felis sp.  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)..(429)  
;; OTHER INFORMATION: coding sequence of 3R4 feline GM-CSF gene  
US-09-617-594A-9

Query Match 76.1%; Score 331.2; DB 3; Length 432;  
Best Local Similarity 85.4%; Pred. No. 1.8e-87;  
Matches 369; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
  
QY 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 60  
DB |||||  
QY 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 60  
DB |||||  
QY 61 CGCCAAACCAGCCCTGTCTACCTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
DB |||||  
QY 61 AGTTCACCCAGCTCTGTCTACCTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
DB |||||  
QY 121 AGCCTTCTGAACACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180  
DB |||||  
QY 121 AGCCTTCTGAACACAGTAGTGAAATAACTGCTGTGATGAATGAAGCAGTAGAGTCGTC 180  
DB |||||  
QY 181 TCTGAAACCTTTGAGCCGCGAGGAGCTGACATGCCTGCAGACTCGCTGAAAGCTGTACAA 240  
DB |||||  
QY 181 TCTGAAATGTTTGACCCCTGAGGAGCCGAAATGCCCTGCAGACTCACCTAAAGCTGTACGAG 240  
DB |||||  
QY 241 CAGGGCTTGGGGGCGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCAC 300  
DB |||||  
QY 241 CAGGGCTTACGGGCGAGGCTCATCAGCCTCAAGGAGCCTCTGAGGATGATGGCCAGCAT 300  
DB |||||  
QY 301 TACAAGCAGCACTGCCCCCGCCCTTACTTCCCGAAACGCCCTGTGAAACCCAGACTATCACCTTC 360  
DB |||||  
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420  
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QY 421 CCAGCCAGCAAG 432  
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QY 421 CCAGTCAAGAG 432  
DB |||||

RESULT 12  
US-10-209-507-9  
; Sequence 9, Application US/10209507  
; Patent No. 6914134  
; GENERAL INFORMATION:  
; APPLICANT: Audonnet, et al.  
; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V  
; FILE REFERENCE: 454313-3151.2  
; CURRENT APPLICATION NUMBER: US/10/209,507  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: 09/617,594  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/193,332  
; PRIOR FILING DATE: 2000-03-30

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; PRIOR APPLICATION NUMBER: France 00 01761
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: France 99 09421
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Felis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(429)
; OTHER INFORMATION: coding sequence of 3R4 feline GM-CSF gene
US-10-209-507-9

Query Match          76.1%; Score 331.2; DB 3; Length 432;
Best Local Similarity 85.4%; Pred. No. 1.8e-87;
Matches 369; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAGAACTGCTTCTCTGGGCACCTGTGTTTACAGCATGCCCGCACCACC 60
Db 1 ATGTGCTGCAGAACTGCTTCTCTGGGCACCTGTGTTTACAGCATCTCTGCACCACC 60

QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 120
Db 61 AGTTCACCCAGCTCTGTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGGAGCTCTG 120

QY 121 AGCCTTCTGAAACAACAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 AGCCTTCTGAAACAACAGTAGTAACTGCTGTATGAATGAACAGTAGAAGTCGTC 180

QY 181 TCTGAAAGCTTTGACCGCGAGGAGCTGACATCGCTGCAGACTCGCTGAAGCTGTACAA 240
Db 181 TCTGAAAGCTTTGACCGCGAGGAGGAAATGCTGCAGACTCACCTAAAGCTGTACAG 240

QY 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGAGGATGATGCCAACCAT 300

QY 301 TACAAGCAGCACTGCCGCCCAACCTTCTGTGAACTTCTGTGCAACCCAGATGATCATTTC 360
Db 301 TACAAGCAGCACTGCCGCCCAACCTTCTGTGAACTTCTGTGCAACCCAGATGATCATTTC 360

QY 361 AAAAGTTTCARAAAGAACTGAAAGATTTCTGTTTGAGATCCGTTTGACTGCTGGAG 420
Db 361 AAAAGTTTCARAAAGAACTGAAAGATTTCTGTTTGAGATCCCTTTTACTCCCTTTGACTGCTGGAG 420

QY 421 CCAGCCCAAGAG 432
Db 421 CCAGTCAAGAG 432
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RESULT 13

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US-08-848-760B-8
; Sequence 8, Application US/08848760B
; Patent No. 6248721
; GENERAL INFORMATION:
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: United States of America
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,760B
; FILING DATE: 25-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,701
; FILING DATE: 09-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PACE, DORAN R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: CNG-i00C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-848-760B-8

Query Match          76.1%; Score 331; DB 3; Length 435;
Best Local Similarity 85.1%; Pred. No. 2e-87;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAGAACTGCTTCTCTGGGCACCTGTGTTTACAGCATGCCCGCACCACC 60
Db 1 ATGTGCTGCAGAGCTGCTGCTCTTGGGCACCTGTGCGCCTGCAGCATCTCTGCACCCGCC 60

QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG 120
Db 61 CGCTCGCCAGCCCGCAGCAGCGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG 120

QY 121 AGCCTTCTGAAACAACAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 CGTCTCTGAACTCAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180

QY 181 TCTGAAAGCTTTGACCGCGAGGAGCTGACATCGCTGCAGACTCGCTGAAGCTGTACAA 240
Db 181 TCAGAAATGTTTGAACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAGCTGTACAAG 240

QY 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTGGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTGGAAGGCCCTTGACCATGATGCCAGCCAC 300

QY 301 TACAAGCAGCACTGCCGCCCAACCTTCTGTGCAACCCAGATGATCATTTC 360
Db 301 TACAAGCAGCACTGCCCTCCAAACCCCGGAAACTTCTGTGCAACCCAGATGATCATTTC 360

QY 361 AAAAGTTTCARAAAGAACTGAAAGATTTCTGTTTGAGATCCGTTTGACTGCTGGAG 420
Db 361 GAAAGTTTCARAAAGAACTGAAAGACTTCTGCTGTGTCATCCCTTTGACTGCTGGAG 420

QY 421 CCAGCCCAAGAGTAA 435
Db 421 CCAGTCCAGGAGTGA 435
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RESULT 14

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US-09-826-025-8
; Sequence 8, Application US/09826025
; Patent No. 6730512
; GENERAL INFORMATION:
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Combination Immunogene Therapy
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
```



;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 94104  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/826,025  
;; FILING DATE: 04-Apr-2001  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/838,702  
;; FILING DATE: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ingolia, Diane E.  
;; REGISTRATION NUMBER: 40,027  
;; REFERENCE/DOCKET NUMBER: CHANG-02687  
;;  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 705-8410  
;; TELEFAX: (415) 397-8338  
;;  
;; INFORMATION FOR SEQ ID NO: 8:  
;;  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 435 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;;  
;; MOLECULE TYPE: other nucleic acid  
;; DESCRIPTION: /desc = "DNA"  
;;  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-826-025-8

Query Match 76.1%; Score 331; DB 3; Length 435;  
Best Local Similarity 85.1%; Pred. No. 2e-87;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
  
QY 1 ATGTGGCTCGAAGACCTGCTCTTCTGGGCACTGTGGTTTACAGCATGCCGACCCACC 60  
Db |||||  
QY 1 ATGTGGCTCGAGAGCTGCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 60  
Db |||||  
QY 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGCGAGCATGTGGATGCCATCAAGGAGCCCTG 120  
Db |||||  
QY 61 CGCTGCCAGCCCGAGCAGCGAGCCCTGGGAGCATGTGAATGCCATCAGAGGCCCG 120  
Db |||||  
QY 121 AGCCTTCTGAACAAACAGTAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
Db |||||  
QY 121 CGTCTCTGAACCTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180  
Db |||||  
QY 181 TCTGAACCTTTGACGCCGAGAGCTGACATGCTGTCGACACTGCGCTGAAGCTGTACAA 240  
Db |||||  
QY 181 TCAGAAATGTTGACCTCCAGGAGCGAGCTGCCTACAGACCCGCTGGAGCTGTACAA 240  
Db |||||  
QY 241 CAGGCTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
Db |||||  
QY 241 CAGGCTTCGGGGGAGCCCTCACCAAGCTCAAGGCCCTTGACCATGATGCCAGCCAC 300  
Db |||||  
QY 301 TACAAGCAGCACTGCCCGCCCGCCCTCTGCTGAAACTTCTGTGCAACCCAGATGATCACTTC 360  
Db |||||  
QY 301 TACAAGCAGCACTGCCCTCCACCCCGGAACTTCTGTGCAACCCAGATGATCACTTC 360  
Db |||||  
QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTTGTGTTGAGATCCCGTTTGAAGCTGTGGAG 420  
Db |||||  
QY 361 GAAAGTTTCAAAAGAACCTGAAGGATTTTGTGTTGATCCCGTTTGAAGCTGTGGAG 420  
Db |||||  
QY 421 CCAGCCCAAGAGTAA 435  
Db |||||  
QY 421 CCAGTCCAGGAGTGA 435  
Db |||||

RESULT 15

US-09-543-679A-2706

;; Sequence 2706, Application US/09543679A  
;; Patent No. 7034007  
;; GENERAL INFORMATION:  
;; APPLICANT: NYCE, Jonathan W.  
;; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,  
;; COMPOSITIONS, KIT & METHOD FOR TREATMENT  
;; OF AIRWAY DISORDERS ASSOCIATED WITH  
;; BRONCHOCONSTRICTION, LUNG INFLAMMATION,  
;;  
;; NUMBER OF SEQUENCES: 3111  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
;; STREET: 7 Clarke Drive  
;; CITY: Cranbury  
;; STATE: NJ  
;; COUNTRY: USA  
;; ZIP: 08512  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: CD-R  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: N/A  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/543,679A  
;; FILING DATE: 13-Apr-2000  
;; CLASSIFICATION: UNKNOWN  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/127,958  
;; FILING DATE: 1998-08-03  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Amzel, Viviana  
;; REGISTRATION NUMBER: 30,930  
;; REFERENCE/DOCKET NUMBER: EPI-0067191b  
;;  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 609-409-3035  
;; TELEFAX: 413-254-9245  
;;  
;; INFORMATION FOR SEQ ID NO: 2706:  
;;  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 789 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2706  
US-09-543-679A-2706

Query Match 76.1%; Score 331; DB 5; Length 789;  
Best Local Similarity 85.1%; Pred. No. 2.6e-87;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
  
QY 1 ATGTGGCTGCAGAACCTGCTCTTCTGGGCACTGTGGTTTACAGCATGCCGACCCACC 60  
Db |||||  
QY 33 ATGTGGCTGCAGAGCTGCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 92  
Db |||||  
QY 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGCGAGCATGTGGATGCCATCAAGGAGCCCTG 120  
Db |||||  
QY 93 CGCTGCCAGCCCGAGCAGCGAGCCCTGGGAGCATGTGAATGCCATCAGAGGCCCG 152  
Db |||||  
QY 121 AGCCTTCTGAACAAACAGTAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
Db |||||  
QY 153 CGTCTCTGAACCTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 212  
Db |||||  
QY 181 TCTGAACCTTTGACGCCGAGGAGCTGACATGCCCTGCGAGACTCGCTGAAGCTGTACAA 240  
Db |||||  
QY 213 TCAGAAATGTTTGAACCTCCAGGAGCGAGCTGCCTACAGACCCGCTGGAGCTGTACAA 272  
Db |||||  
QY 241 CAGGCTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
Db |||||  
QY 273 CAGGCTTCGGGGGAGCCCTCACCAAGCTCAAGGCCCTTGACCATGATGCCAGCCAC 332  
Db |||||  
QY 301 TACAAGCAGCACTGCCCGCCCGCCCTGCTGCAACTTCTGTGCAACCCAGATGATCACTTC 360  
Db |||||  
QY 333 TACAAGCAGCACTGCCCTCCCAACCCCGGAACTTCTGTGCAACCCAGATGATCACTTC 392  
Db |||||



Qy	361	AAAAGTTTCAAAAAGAACTCTAAGGATTTTCTGTTTGAGATCCCGTTTGA	CTCTGGAG	420
Db	393	GAAAGTTTCAAAAGAGAACTCTAAGGACTTTCTGCTTGT	CATCCCCCTTTGACTCTGGAG	452
Qy	421	CCAGCCCCAAGAGTAA	435	
Db	453	CCAGTCCAGGAGTGA	467	

Search completed: May 26, 2006, 01:29:01  
Job time : 166 secs

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 01:24:10 ; Search time 1032 Seconds  
(without alignments)  
5179.381 Million cell updates/sec

Title: US-10-614-481-8  
Perfect score: 435  
Sequence: 1 atgtggctgcagaaactgct.....ggaagccagccagagtaa 435

Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	10	US-10-614-481-8
2	332.6	76.5	444	6	US-10-218-654-119
3	332.6	76.5	444	6	US-10-218-654-121
4	332.6	76.5	444	7	US-10-262-439-119
5	332.6	76.5	444	7	US-10-262-439-121
6	331.2	76.1	432	6	US-10-209-507-9
7	331	76.1	435	3	US-09-826-025-8
8	331	76.1	435	6	US-10-083-590-14
9	331	76.1	435	8	US-10-411-037-17
10	331	76.1	435	8	US-10-411-026-17
11	331	76.1	435	8	US-10-410-962-17
12	331	76.1	435	8	US-10-411-049-17
13	331	76.1	435	8	US-10-410-930-17
14	331	76.1	435	8	US-10-410-997-17
15	331	76.1	435	8	US-10-411-012-17
16	331	76.1	435	8	US-10-287-994-17
17	331	76.1	435	8	US-10-410-913-17

18	331	76.1	435	9	US-10-785-377-8	Sequence 8, Appli
19	331	76.1	435	9	US-10-410-380-17	Sequence 17, Appl
20	331	76.1	435	10	US-10-410-897-17	Sequence 17, Appl
21	331	76.1	435	10	US-10-492-261-17	Sequence 17, Appl
22	331	76.1	435	11	US-10-937-658-2	Sequence 2, Appli
23	331	76.1	435	16	US-11-183-205-17	Sequence 17, Appl
24	331	76.1	435	16	US-11-201-384-16	Sequence 16, Appl
25	331	76.1	448	8	US-10-609-346-19	Sequence 19, Appl
26	331	76.1	781	8	US-10-447-315-20	Sequence 20, Appl
27	331	76.1	789	7	US-10-131-985-16	Sequence 16, Appl
28	331	76.1	789	9	US-10-901-417-16	Sequence 16, Appl
29	331	76.1	900	10	US-10-925-205-10	Sequence 10, Appl
30	331	76.1	900	15	US-11-066-480-10	Sequence 10, Appl
31	331	76.1	1172	10	US-10-925-205-5	Sequence 5, Appli
32	331	76.1	1172	15	US-11-066-480-5	Sequence 5, Appli
33	329.6	75.8	432	6	US-10-218-654-122	Sequence 122, App
34	329.6	75.8	432	6	US-10-218-654-123	Sequence 123, App
35	329.6	75.8	432	6	US-10-209-507-7	Sequence 7, Appli
36	329.6	75.8	432	7	US-10-262-439-122	Sequence 123, App
37	329.6	75.8	432	7	US-10-262-439-123	Sequence 123, App
38	329.6	75.8	1833	3	US-09-783-708-2	Sequence 2, Appli
39	329.4	75.7	435	7	US-10-188-056-32	Sequence 32, Appli
40	329.4	75.7	435	10	US-10-775-204-15	Sequence 15, Appl
41	329.4	75.7	435	10	US-10-775-204-16	Sequence 16, Appl
42	329.4	75.7	435	10	US-10-775-204-108	Sequence 108, App
43	329.4	75.7	435	10	US-10-775-204-109	Sequence 109, App
44	329.4	75.7	496	7	US-10-267-384-191	Sequence 191, App
45	329.4	75.7	505	9	US-10-688-845-82	Sequence 82, Appl

## ALIGNMENTS

## RESULT 1

US-10-614-481-8  
; Sequence 8, Application US/10614481  
; Publication No. US20050059121A1  
; GENERAL INFORMATION:  
; APPLICANT: Bublot, et al.  
; TITLE OF INVENTION: Equine GM-CSF  
; FILE REFERENCE: 454313-2334.1  
; CURRENT APPLICATION NUMBER: US/10/614,481  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: US/09/589,460  
; PRIOR FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: 60/138,843  
; PRIOR FILING DATE: 1999-06-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 435  
; TYPE: DNA  
; ORGANISM: Equine sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(432)  
; OTHER INFORMATION: coding sequence of equine GM-CSF gene  
US-10-614-481-8

Query Match 100.0%; Score 435; DB 10; Length 435;  
Best Local Similarity 100.0%; Pred. No. 8.7e-131;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGTGGCTGCAGAACTGCTCTTCTTGGGCACTGGTTTACAGCATGCCACCCACC 60
Db	1	ATGTGGCTGCAGAACTGCTCTTCTTGGGCACTGGTTTACAGCATGCCACCCACC 60
Qy	61	CGCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGGATGCCATCAAGGAGGCCCTG 120
Db	61	CGCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGGATGCCATCAAGGAGGCCCTG 120
Qy	121	AGCCTTCTTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAATGCTC 180

Db 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAGTCGTC 180  
Qy 181 TCTGAAACGTTTGAACGCGAGAGCTGACATGCTCTGCAGACTCGCTGAAGCTGTACAAA 240  
Db 181 TCTGAAACGTTTGAACGCGAGAGCTGACATGCTCTGCAGACTCGCTGAAGCTGTACAAA 240  
Qy 241 CAGGCTTGGGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300  
Db 241 CAGGCTTGGGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300  
Qy 301 TACAAGCAGCAGCTGCCCCCAACCTCGAACTTCTGTGCAACCCAGATGATCACTTC 360  
Db 301 TACAAGCAGCAGCTGCCCCCAACCTCGAACTTCTGTGCAACCCAGATGATCACTTC 360  
Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGTGGAG 420  
Db 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGTGGAG 420  
Qy 421 CCAGCCCAAGTAA 435  
Db 421 CCAGCCCAAGTAA 435

## RESULT 2

US-10-218-654-119  
; Sequence 119, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 119  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Felis catus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)...(441)  
US-10-218-654-119

Query Match 76.5%; Score 332.6; DB 6; Length 444;  
Best Local Similarity 85.3%; Pred. No. 2.1e-97;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
Qy 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60  
Db 10 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 69  
Qy 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
Db 70 AGTTCAACCCAGCTGTCTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGGAGGCCCTG 129  
Qy 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180  
Db 130 AGCCTTCTGAACAACAGTAGTAGTAATACTGCTGTATGAATGAAGCAGTAGAGTCGTC 189  
Qy 181 TCTGAAACGTTTGAACGCGAGAGCTGACATGCCCTGCAGACTCGCTGAAGCTGTACAAA 240  
Db 190 TCTGAAATGTTTGAACCTGAGAGCCGAAATGCCCTGCAGACTCACCTAAAGCTGTACGAG 249  
Qy 241 CAGGCTTGGGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300

Db 250 CAGGCTTACGGGAGAGCTCATCAGCTCAAGAGCCTCTGAGATGATGAGCCAAACCAT 309  
Qy 301 TACAAGCAGCAGCTGCCCCCAACCTCGAACTTCTCTGTGCAACCCAGATGATCACTTC 360  
Db 310 TACAAGCAGCAGCTGCCCCCTTACTCCGAAACGCCCTGTGAAACCCAGACTATCACTTC 369  
Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGTGGAG 420  
Db 370 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTAAACAACCCCTTTGACTGTGGGA 429  
Qy 421 CCAGCCCAAGTAA 435  
Db 430 CCAGCCCAAGTAA 444

## RESULT 3

US-10-218-654-121/c  
; Sequence 121, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 121  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Felis catus  
US-10-218-654-121

Query Match 76.5%; Score 332.6; DB 6; Length 444;  
Best Local Similarity 85.3%; Pred. No. 2.1e-97;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
Qy 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60  
Db 435 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 376  
Qy 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120  
Db 375 AGTTCAACCCAGCTGTCTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGGAGGCCCTG 316  
Qy 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180  
Db 315 AGCCTTCTGAACAACAGTAGTAGTAATACTGCTGTATGAATGAAGCAGTAGAGTCGTC 256  
Qy 181 TCTGAAACGTTTGAACGCGAGAGCTGACATGCCCTGCAGACTCGCTGAAGCTGTACAAA 240  
Db 255 TCTGAAATGTTTGAACCTTGAGAGCCGAAATGCCCTGCAGACTCACCTAAAGCTGTACGAG 196  
Qy 241 CAGGCTTGGGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300  
Db 195 CAGGCTTACGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 136  
Qy 301 TACAAGCAGCAGCTGCCCCCAACCTCGAACTTCTGTGCAACCCAGATGATCACTTC 360  
Db 135 TACAAGCAGCAGCTGCCCCCTTACTCGAAGAGCCCTGTGAAACCCAGACTATCACTTC 76  
Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGTGGAG 420  
Db 75 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTAAACAACCCCTTTGACTGTGGGA 16

QY 421 CCAGCCCAAGTAA 435  
Db 15 CCAGACCAGAGTAA 1

RESULT 4  
US-10-262-439-119  
; Sequence 119, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Ke  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 119  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Felis catus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)..(441)  
US-10-262-439-119

Query Match 76.5%; Score 332.6; DB 7; Length 444;  
Best Local Similarity 85.3%; Pred. No. 2.1e-97;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTGTACAGCATGCCGACCCACC 60  
Db 10 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTGTACAGCATCTCTGCACCCACC 69

QY 61 CGCCAAACCCAGCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
Db 70 AGTTCAACCCAGCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 129

QY 121 AGCCTTCTGAAACAAGTAGTGACATGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
Db 130 AGCCTTCTGAAACAAGTAGTGAAATACTGTGTGATGAATGAACAGTAGAAGTCGTC 189

QY 181 TCTGAAACCTTTGACCCGAGGAGTGACATGCTGTGACAGCTCGCTGAAGCTGTACAA 240  
Db 190 TCTGAAATGTTTGACCTGAGGAGCGAAATGCTGTGACAGCTCACCTAAAGCTGTACGAG 249

QY 241 CAGGGCTTCGGGGGAGCCTCATCAGCTCGAAGGCCCTTGACCATGTATGCCAGCCAC 300  
Db 250 CAGGGCTTCAGGGGAGCCTCATCAGCTCGAAGGCCCTTGAGATGTATGCCAACCAT 309

QY 301 TACAAGCAGACTGCCCCCCCCCTTCTGTGCAACCCAGATGATCAGCTTC 360  
Db 310 TACAAGCAGACTGCCCCCTTACTCGGAAAGCCCTGTGAAACCCAGACTATCAGCTTC 369

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTCTGTGTGATCCCGTTTCACTGCTGAAG 420  
Db 370 AAAATTTTCAAAAGAACTCTGAAGGATTTCTGTGTGATTTTAAACCCCTTTGACTGCTGGGA 429

QY 421 CCAGCCCAAGTAA 435  
Db 430 CCAGACCAGAGTAA 444

RESULT 5  
US-10-262-439-121/c  
; Sequence 121, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Ke  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 121  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Felis catus  
; ORGANISM: Felis catus  
US-10-262-439-121

Query Match 76.5%; Score 332.6; DB 7; Length 444;  
Best Local Similarity 85.3%; Pred. No. 2.1e-97;  
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTGTACAGCATGCCGACCCACC 60  
Db 435 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTGTACAGCATCTCTGCACCCACC 376

QY 61 CGCCAAACCCAGCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
Db 375 AGTTCAACCCAGCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 316

QY 121 AGCCTTCTGAAACAAGTAGTGACATGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
Db 315 AGCCTTCTGAAACAAGTAGTGAAATACTGTGTGATGAATGAACAGTAGAAGTCGTC 256

QY 181 TCTGAAACCTTTGACCCGAGGAGTGACATGCTGTGACAGCTCGCTGAAGCTGTACAA 240  
Db 255 TCTGAAATGTTTGACCCCTGAGGAGCGAAATGCTGTGACAGCTCACCTAAAGCTGTACGAG 196

QY 241 CAGGGCTTCGGGGGAGCCTCATCAGCTCGAAGGCCCTTGACCATGTATGCCAGCCAC 300  
Db 195 CAGGGCTTCAGGGGAGCCTCATCAGCTCGAAGGCCCTTGAGATGTATGCCAACCAT 136

QY 301 TACAAGCAGACTGCCCCCCCCCTTCTGTGCAACCCAGATGATCAGCTTC 360  
Db 135 TACAAGCAGACTGCCCCCTTACTCGGAAAGCCCTGTGAAACCCAGACTATCAGCTTC 76

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTCTGTGTGATCCCGTTTCACTGCTGAAG 420  
Db 75 AAAATTTTCAAAAGAACTCTGAAGGATTTCTGTGTGATTTTAAACCCCTTTGACTGCTGGGA 16

QY 421 CCAGCCCAAGTAA 435  
Db 15 CCAGACCAGAGTAA 1

RESULT 6  
US-10-209-507-9  
; Sequence 9, Application US/10209507  
; Publication No. US20030109033A1  
; GENERAL INFORMATION:  
; APPLICANT: Audonnet, et al.  
; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V

FILE REFERENCE: 454313-3151.2  
CURRENT APPLICATION NUMBER: US/10/209,507  
CURRENT FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: 09/617,594  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/193,332  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: France 00 01761  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: France 99 09421  
PRIOR FILING DATE: 1999-07-16  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 9  
LENGTH: 432  
TYPE: DNA  
ORGANISM: Felis sp.  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(429)  
OTHER INFORMATION: coding sequence of 3R4 feline GM-CSF gene  
US-10-209-507-9

Query Match 76.1%; Score 331.2; DB 6; Length 432;  
Best Local Similarity 85.4%; Pred. No. 6e-97;  
Matches 369; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60  
Db 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60

QY 61 CGCAACCCAGCCCTGCTACTCGGCCCTGGGAGCATGTGGATGCCATCAAGAGGCCCTG 120  
Db 61 AGTTCAACCCAGCTGCTCACTCGGCCCTGGCAACAGCTGGATGCCATCAAGAGGCCCTG 120

QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
Db 121 AGCCTTCTGAACAACAGTAGTGAAATACTGCTGTATGAATGAAGAGTAGAAGTCGTC 180

QY 181 TCTGAACGTTTGACCGCCGAGGAGCTGACATGCCCTGCAGACTCGCTGAAGCTGTACAA 240  
Db 181 TCTGAACGTTTGACCGCTGAGGAGCGGAAATGCCCTGCAGACTCACTAAAGCTGTACAG 240

QY 241 CAGGCTTTCGGGGGAGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
Db 241 CAGGCTTTCGGGGGAGCTCATCAAGCTCGAAGGCCCTTGAGGATGATGCCCAACCAT 300

QY 301 TACAAGCAGACTGCCCCCACCCTGGAACTTCTGTGCAACCCAGATGATCACTTC 360  
Db 301 TACAAGCAGACTGCCCCCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 360

QY 361 AAAAGTTTCAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAG 420  
Db 361 AAAAATTTCAAGAGAACTGAAGGATTTCTGTGTTTAAATCCCTTTGACTGTCTGGAA 420

QY 421 CCAGCCGAGAAG 432  
Db 421 CCAGTCAAGAAG 432

RESULT 7  
US-09-826-025-8  
Sequence 8, Application US/09826025  
Patent No. US20020162123A1  
GENERAL INFORMATION:  
APPLICANT: Chang, Lung-Ji  
TITLE OF INVENTION: Combination Immunogene Therapy  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California

COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/826,025  
FILING DATE: 04-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/838,702  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: CHANG-02687  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 435 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-826-025-8

Query Match 76.1%; Score 331; DB 3; Length 435;  
Best Local Similarity 85.1%; Pred. No. 7e-97;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60  
Db 1 ATGTGGCTGCAGAGCTGCTGCTCTTGGGCACTGTGGCTTGAGGATCTCTGCACCCGCC 60

QY 61 CGCAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120  
Db 61 CGCTCGCCAGCCCGCAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120

QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180  
Db 121 CGTCTCTGAACTCTGAGTAGAGACACTGCTGTGATGAATGAACAGTAGAAGTCATC 180

QY 181 TCTGAACGTTTGACCGCGAGGAGCTGACATGCCCTGCAGACTCGCTGAAGCTGTACAA 240  
Db 181 TCAGAAATGTTTGACCTCGAGGAGCGACCTGCTTACAGACCCGCTGGAGCTGTACAG 240

QY 241 CAGGCTTTCGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300  
Db 241 CAGGCTTTCGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGAGGAGCCCTTGACCATGATGCCAGCCAC 300

QY 301 TACAAGCAGACTGCCCCCACCCTGGAACTTCTGTGTTGAGATCCCGTTTGACTGTGGAG 360  
Db 301 TACAAGCAGACTGCCCCCTTCAACCCCGGAACTTCTGTGTTGAGATCCCGTTTGACTGTGGAG 360

QY 361 AAAAGTTTCAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAG 420  
Db 361 GAAAGTTTCAAAAGAACTGAAGGATTTCTGTGTTGATCCCGTTTGACTGTGGAG 420

QY 421 CCAGCCGAGAAGTAA 435  
Db 421 CCAGTCCAGGAGTGA 435

RESULT 8  
US-10-083-590-14  
Sequence 14, Application US/10083590  
Publication No. US20030027257A1



```
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-026-17
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Query Match 76.1%; Score 331; DB 8; Length 435;
Best Local Similarity 85.1%; Pred. No. 7e-97;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGACCCACC 60
DB 1 ATGTGCTGCAAGAACCTGCTTCTTGGGCACTGTGGTTTACAGCATGCCGACCCGCC 60

QY 61 CGCCAAACCCAGCCCTGCTCACTGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB 61 CGCTCGCCAGCCCGCCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120

QY 121 AGCCTTCTGAACAAAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
DB 121 CGTCTCTGAACTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180

QY 181 TGTAAACCTTTGAACCCGAGGAGTGACATGCTGCTGACAGCTCGCTGAAAGCTGTACAA 240
DB 181 TCAGAAATGTTTGAACCTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 240

QY 241 CAGGGCTTGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
DB 241 CAGGGCTTGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300

QY 301 TACAAGCAGCACTGCCCCCAGCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTTC 360
DB 301 TACAAGCAGCACTGCCCCCAGCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTTC 360

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG 420
DB 361 GAAAGTTTCAAAAGAACCTGAAGGATTTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG 420

QY 421 CCAGCCCAAGAGTAA 435
DB 421 CCAGTCCAGGAGTGA 435
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RESULT 11
US-10-410-962-17
; Sequence 17, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Niose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
```

```
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Caryn
; TITLE OF INVENTION: GLYCOCONJUGATE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-962-17
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Query Match 76.1%; Score 331; DB 8; Length 435;
Best Local Similarity 85.1%; Pred. No. 7e-97;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGACCCACC 60
DB 1 ATGTGCTGCAAGAACCTGCTTCTTGGGCACTGTGGTTTACAGCATGCCGACCCGCC 60

QY 61 CGCCAAACCCAGCCCTGCTCACTGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB 61 CGCTCGCCAGCCCGCCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120

QY 121 AGCCTTCTGAACAAAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
DB 121 CGTCTCTGAACTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180

QY 181 TGTAAACCTTTGAACCCGAGGAGTGACATGCTGCTGACAGCTCGCTGAAAGCTGTACAA 240
DB 181 TCAGAAATGTTTGAACCTCAGGAGCCGACCTGCTTACAGACCCGCTGAGCTGTACAA 240

QY 241 CAGGGCTTGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
DB 241 CAGGGCTTGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300

QY 301 TACAAGCAGCACTGCCCCCAGCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTTC 360
DB 301 TACAAGCAGCACTGCCCCCAGCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTTC 360

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG 420
DB 361 GAAAGTTTCAAAAGAACCTGAAGGATTTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG 420

QY 421 CCAGCCCAAGAGTAA 435
DB 421 CCAGTCCAGGAGTGA 435
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RESULT 12
US-10-411-049-17
; Sequence 17, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
```



APPLICANT: Neose Technologies, Inc.  
APPLICANT: DeFrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bove, Caryn  
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
TITLE OF INVENTION: ALPHA  
FILE REFERENCE: 040853-01-5055  
CURRENT APPLICATION NUMBER: US/10/411,049  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 17  
LENGTH: 435  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-411-049-17

Query Match 76.1%; Score 331; DB 8; Length 435;  
Best Local Similarity 85.1%; Pred. No. 7e-97;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy	1	ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCCGACCCACC 60
Db	1	ATGTGGCTGCAGAGCTGCTGCTTCTGGGCACCTGTTGGGCATGTGGCTGCAGCATCTCTGCACCCGCC 60
Qy	61	CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db	61	CGCTCGCCCGAGCCCGAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120
Qy	121	AGCCTTCTGAACCAACAGTAGTGACACTGCTGCTATCATGAATGAACACAGTAGAAGTCGTC 180
Db	121	CGTCTCTGAACTCGAGTAGAGACACTGCTGCTGAGATGAATGAACACAGTAGAAGTCATC 180
Qy	181	TCTGAAACGTTTGAGCCCGAGGAGCTGACATGCCCTGCAGACTCGGCTGAAGCTGTACAAA 240
Db	181	TCAGAAATGTTTGACTCCAGAGCCGACCTGCTGCATACAGACCCGCTGGAGCTGTACAA 240
Qy	241	CAGGCTTCGCGGGGAGCTCATCAAGCTCGAAGGCCCTTCACCATGATGCGCAGCCAC 300
Db	241	CAGGCTTCGCGGGGAGCTCATCAAGCTCGAAGGCCCTTCACCATGATGCGCAGCCAC 300
Qy	301	TACAAAGCAGCACTGCCCCCCCCCACTTCTGTGCAACCCAGATGATACCTTC 360
Db	301	TACAAAGCAGCACTGCCCCCCCCCACTTCTGTGCAACCCAGATGATACCTTC 360
Qy	361	AAAAGTTTCAAAAGAACCTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
Db	361	AAAAGTTTCAAAAGAACCTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
Qy	421	CCAGCCCAAGTAA 435
Db	421	CCAGTCCAGGAGTGA 435

RESULT 13  
US-10-410-930-17

Sequence 17, Application US/10410930  
Publication No. US20040115168A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: DeFrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bove, Caryn  
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
TITLE OF INVENTION: BETA  
FILE REFERENCE: 040853-01-5056  
CURRENT APPLICATION NUMBER: US/10/410,930  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 17  
LENGTH: 435  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-410-930-17

Query Match 76.1%; Score 331; DB 8; Length 435;  
Best Local Similarity 85.1%; Pred. No. 7e-97;  
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy	1	ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCCGACCCACC 60
Db	1	ATGTGGCTGCAGAGCTGCTGCTTCTGGGCACCTGTTGGGCATGTGGCTGCAGCATCTCTGCACCCGCC 60
Qy	61	CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db	61	CGCTCGCCCGAGCCCGAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120
Qy	121	AGCCTTCTGAACCAACAGTAGTGACACTGCTGCTATCATGAATGAACACAGTAGAAGTCGTC 180
Db	121	CGTCTCTGAACTCGAGTAGAGACACTGCTGCTGAGATGAATGAACACAGTAGAAGTCATC 180
Qy	181	TCTGAAACGTTTGAGCCCGAGGAGCTGACATGCCCTGCAGACTCGGCTGAAGCTGTACAAA 240
Db	181	TCAGAAATGTTTGACTCCAGAGCCGACCTGCTGCATACAGACCCGCTGGAGCTGTACAA 240
Qy	241	CAGGCTTCGCGGGGAGCTCATCAAGCTCGAAGGCCCTTCACCATGATGCGCAGCCAC 300
Db	241	CAGGCTTCGCGGGGAGCTCATCAAGCTCGAAGGCCCTTCACCATGATGCGCAGCCAC 300
Qy	301	TACAAAGCAGCACTGCCCCCCCCCACTTCTGTGCAACCCAGATGATACCTTC 360
Db	301	TACAAAGCAGCACTGCCCCCCCCCACTTCTGTGCAACCCAGATGATACCTTC 360
Qy	361	AAAAGTTTCAAAAGAACCTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
Db	361	AAAAGTTTCAAAAGAACCTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
Qy	421	CCAGCCCAAGTAA 435
Db	421	CCAGTCCAGGAGTGA 435

RESULT 14  
US-10-410-997-17  
; Sequence 17, Application US/10410997  
; Publication No. US20040126838A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DePrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bove, Caryn  
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF  
; TITLE OF INVENTION: FSH  
; FILE REFERENCE: 040853-01-5059  
; CURRENT APPLICATION NUMBER: US/10/410,997  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 435  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-410-997-17

Query Match	76.1%; Score 331; DB 8; Length 435;
Best Local Similarity	85.1%; Pred. No. 7e-97;
Matches 370; Conservative	0; Mismatches 65; Indels 0; Gaps 0;
QY	1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATCCCGCACCCACC 60
DB	1 ATGTGGCTGCAGAGCTGCTCTTGGGCACTGTGGCTCGAGCATCTCTGCACCCGCC 60
QY	61 CGCCAAACCCAGCCCTGTGCATCGGCCCTGGCAGCATGTGGATGCCATCAAGAGAGCCCTG 120
DB	61 CGCTCGCCACGCCCCAGCACGCGAGCCCTGGGAGCATGTGAATGCCATCCAGAGAGCCCGG 120
QY	121 AGCCTTCTGAAACAACAGTAGTGCACATGCTGCTATCATGAATGAAACAGTAGAAGTGC 180
DB	121 CGTCTCTGAAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCA 180
QY	181 TCTGAAACGGTTTGACGCCGAGGAGCTGACATGCCTGCGAGACTCGCCTGAAGCTGTACAAA 240
DB	181 TCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCGCTGGAGCTGTACAA 240
QY	241 CAGGCTTGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCAGCCAC 300
DB	241 CAGGCTTGGGGGAGGCTCACCAGGCTCAAGGCGCCCTTGACCATGATGGCAGCCAC 300
QY	301 TACAAGCAGCACTGCCCCCCCCACCCCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
DB	301 TACAAGCAGCACTGCCCTCCAAACCCCGAAACTTCTGTGCAACCCAGATTTATCACCTTT 360
QY	361 AAAAGTTTCAAAAGAACTGAAGGATTTCTGTTTGAATGCCCTTTGACTGCTGGAAG 420
DB	361 GAAAGTTTCAAAAGAACTGAAGGACTTTCTGCTTGTGATCTCCCTTTGACTGCTGGAG 420
QY	421 CCAGCCCCAAGAAGTAA 435

Db 421 CCAGTCCAGGAGTGA 435

RESULT 15  
 US-10-411-012-17  
 ; Sequence 17, Application US/10411012  
 ; Publication No. US20040132640A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: DePrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; APPLICANT: Bowe, Catyue  
 ; TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE  
 ; TITLE OF INVENTION: METHODS  
 ; FILE REFERENCE: 040853-01-5051  
 ; CURRENT APPLICATION NUMBER: US/10/411.012  
 ; CURRENT FILING DATE: 2003-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/328,523  
 ; PRIOR FILING DATE: 2001-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/344,692  
 ; PRIOR FILING DATE: 2001-10-19  
 ; PRIOR APPLICATION NUMBER: US 60/387,292  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/391,777  
 ; PRIOR FILING DATE: 2002-06-25  
 ; PRIOR APPLICATION NUMBER: US 60/396,594  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: US 60/404,249  
 ; PRIOR FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: US 60/407,527  
 ; PRIOR FILING DATE: 2002-08-28  
 ; NUMBER OF SEQ ID NOS: 75  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 17  
 ; LENGTH: 435  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-411-012-17

Query Match	76.1%; Score 331; DB 8; Length 435;
Best Local Similarity	85.1%; Pred. No. 7e-97;
Matches 370; Conservative	0; Mismatches 65; Indels 0; Gaps 0;
QY	1 ATGTGGCTGCAGAACCTGCTTCTTCGGCAGCACTGGTTTACAGCATGCCCGCACCCACC 60       
Db	1 ATGTGGCTGCAGAGCCTGCTCTTGGGCACCTGTGGCCTGCAGCATCTCTGCACCCGCC 60       
QY	61 CGCCAAACCCAGCCCTGTCACTCGGCCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120       
Db	61 CGCTCGCCAGCCCCAGCAGCAGCCCTGGAGCATGTGAATGCCATCCAGGAGGCCCGG 120       
QY	121 AGCCTTCTTGAAACAACAGTAGTGACACTGCTGCTATCATGAATGAAACAGTAGAAGTCGTC 180       
Db	121 CGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATC 180       
QY	181 TCTGAAAAGTTTGAAGCCGAGGAGCTGACATGCTCTGAGACCTCGCTGGAAGCTGTACAAA 240       
Db	181 TCAGAAATGTTTGACCTCCAGGAGCCGACCTCGCCTACAGACCCGCTGGAGCTGTGTACAG 240       
QY	241 CAGGGCTTGGGGGAGCCCTCATCAAGCTGGAAGGCCCTTGACCATGATGCCAGCCAC 300       
Db	241 CAGGGCTTGGGGGAGCGCTCACCAAGCTCAAGGGCCCCCTTGAACATGATGCCAGCCAC 300       
QY	301 TACAAGCAGCACTGCCCCCCCCCACCCTTGAAACTTCTGTGTCAAACCCAGATGATCACCTTC 360       
Db	301 TACAAGCAGCACTGCCCCCTCCNAACCCCGGAAACTTCTGTGTCAAACCCAGATTATCACCTTT 360       
QY	361 AAAAGTTTTCAAAAAAGAACTGAAGGATTTTCTGTGTTGAGATCCCGTTTTGACTGTGTGGAG 420       

Db 361 GAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTGTCATCCCTTTGACTGCTGGGAG 420  
Qy 421 CCAGCCCAAGTAA 435  
Db 421 CCAGTCCAGGAGTGA 435

Search completed: May 26, 2006, 01:41:32  
Job time : 1034 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2006, 15:01:08 ; Search time 50 Seconds  
(without alignments)  
252.088 Million cell updates/sec

Title: US-10-614-481-9

Perfect score: 759

Sequence: 1 MWLQNLLLLGTVVYSPAPTRP.....KNLKDFLFEIPDCWKPAQK 144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pap:\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pap:\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pap:\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pap:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PTUS\_COMB.pap:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	759	100.0	144	2	US-09-589-460-9
2	587	77.3	144	1	US-08-133-979A-11
3	587	77.3	144	1	US-08-436-890-11
4	587	77.3	144	1	US-08-451-213-11
5	586	77.2	144	1	US-08-284-393B-11
6	586	77.2	144	2	US-09-522-217-114
7	586	77.2	144	2	US-09-923-246-114
8	586	77.2	144	2	US-10-295-723-114
9	586	77.2	144	2	US-10-282-622-10
10	586	77.2	144	5	PCT-US95-08950-11
11	586	77.2	334	2	US-09-555-165-9
12	586	77.2	334	2	US-09-555-165-11
13	584	76.9	144	2	US-08-759-628-6
14	578	76.2	143	2	US-09-617-594A-10
15	578	76.2	143	2	US-10-209-507-10
16	577	76.0	143	2	US-09-617-594A-8
17	577	76.0	143	2	US-10-209-507-8
18	576	75.9	144	1	US-08-259-696B-9
19	576	75.9	144	1	US-08-902-513-9
20	571	75.2	144	2	US-09-322-409-120
21	571	75.2	144	2	US-09-451-527-120
22	571	75.2	144	3	US-10-262-439-120
23	570.5	75.2	143	1	US-08-259-696B-10
24	570.5	75.2	143	1	US-08-902-513-10
25	566	74.6	144	1	US-08-259-696B-1
26	566	74.6	144	1	US-08-902-513-1

27	533	70.2	132	7	5229496-4	Patent No. 5229496
28	533	70.2	132	7	5391485-4	Patent No. 5391485
29	532	70.1	168	1	US-08-318-193-10	Sequence 10, Appl
30	532	70.1	782	1	US-09-146-283-4	Sequence 4, Appl
31	532	70.1	782	2	US-08-579-823A-4	Sequence 4, Appl
32	532	70.1	782	2	US-09-344-195-4	Sequence 4, Appl
33	531	70.0	127	7	5405952-2	Patent No. 5405952
34	531	70.0	131	7	5229496-2	Patent No. 5229496
35	531	70.0	301	2	US-08-469-318-142	Sequence 142, App
36	531	70.0	301	2	US-08-468-609A-142	Sequence 142, App
37	531	70.0	301	2	US-08-446-872A-142	Sequence 142, App
38	531	70.0	301	2	US-08-762-227A-142	Sequence 142, App
39	531	70.0	301	5	PCT-US95-01185-142	Sequence 142, App
40	527	69.4	127	1	US-08-318-193-2	Sequence 2, Appl
41	527	69.4	127	2	US-09-462-941-8	Sequence 8, Appl
42	527	69.4	127	7	5229496-15	Patent No. 5229496
43	527	69.4	128	2	US-08-469-318-160	Sequence 160, App
44	527	69.4	128	2	US-08-468-609A-160	Sequence 160, App
45	527	69.4	128	2	US-08-446-872A-160	Sequence 160, App

#### ALIGNMENTS

##### RESULT 1

US-09-589-460-9  
; Sequence 9, Application US/09589460  
; Patent No. 6645740  
; GENERAL INFORMATION:  
; APPLICANT: Bublort, et al.  
; TITLE OF INVENTION: Equine GM-CSF  
; FILE REFERENCE: 454313-2334.1  
; CURRENT APPLICATION NUMBER: US/09/589,460  
; CURRENT FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: 60/138,843  
; PRIOR FILING DATE: 1999-06-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Equine sp.  
US-09-589-460-9

Query Match 100.0%; Score 759; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1.7e-82;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MWLQNLLLLGTVVYSPAPTRPSPVTRPQHVDIAKEALSLNNSSDTAAIMNETVEVV 60

Qy 61 SETFDAELTCLQTLKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120

Db 61 SETFDAELTCLQTLKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120

Qy 121 KSFKKNLKDFLFEIPDCWKPAQK 144

Db 121 KSFKKNLKDFLFEIPDCWKPAQK 144

##### RESULT 2

US-08-133-979A-11  
; Sequence 11, Application US/08133979A  
; Patent No. 5589582  
; GENERAL INFORMATION:  
; APPLICANT: Hawley, Robert J.  
; APPLICANT: Ponath, Paul D.  
; APPLICANT: Rosa, Margaret D.  
; APPLICANT: Monroy, Rodney L.  
; APPLICANT: Schacter, Bernice Z.  
; TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines Therei  
; NUMBER OF SEQUENCES: 24









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; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08950
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,393
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08950-11

Query Match 77.2%; Score 586; DB 5; Length 144;
Best Local Similarity 76.4%; Pred. No. 7.5e-62;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

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Db 1 MWLQNLGLLVVYVSMPTQPSVTRPQWHDVAIKELSLNNSSDTAAIMNETVEV 60
Qy 61 SETFDAELTCLQTRLELYKQGLRSLKLEGPLTMASHYKQHCPTLETSCATQITF 120
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLKLEGPLTMASHYKQHCPTLETSCATQITF 120
Qy 121 KSFKKNLKDFLFEPDCKWPAQK 144
Db 121 ESFKENLKDFLLVIPDCEWPEVQE 144

RESULT 11
US-09-555-165-9
; Sequence 9, Application US/09555165
; Patent No. 6866998
; GENERAL INFORMATION:
; APPLICANT: Kitamura, Toshio
; APPLICANT: Kojima, Tetsuo
; TITLE OF INVENTION: SIGNAL SEQUENCE TRAPPING METHOD
; FILE REFERENCE: 06501-061001
; CURRENT APPLICATION NUMBER: US/09/555,165
; CURRENT FILING DATE: 2000-05-28
; PRIOR APPLICATION NUMBER: JP 9/324912
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: PCT/JP98/05326
; PRIOR FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized human GM-CSF-human mpl
; OTHER INFORMATION: fusion protein sequence
US-09-555-165-11

Query Match 77.2%; Score 586; DB 2; Length 334;
Best Local Similarity 76.4%; Pred. No. 2.6e-61;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

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Qy 121 KSFKKNLKDFLFEPDCKWPAQK 144
Db 121 ESFKENLKDFLLVIPDCEWPEVQE 144

RESULT 13
US-08-759-628-6
; Sequence 6, Application US/08759628
; Patent No. 6225446
; GENERAL INFORMATION:
; APPLICANT: Altman, Scott W.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
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;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,628
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,574
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0552Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 18..144
; OTHER INFORMATION: /note= "peptide of Figure 1"
US-08-759-628-6

Query Match 76.4%; Score 584; DB 2; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.3e-61;
Matches 110; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

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Db 1 MWLQNLGTVVYVSMPTPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
Qy 61 SETFDAELTCLQTRKLYKQGRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQPTCLQTRKLYKQGRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
Qy 121 KSFKNLKDFLFEIPFDCWKPAQ 144
Db 121 ESFKNLKDFLLVIFDCWEPVQE 144

RESULT 14
US-09-617-594A-10
; Sequence 10, Application US/09617594A
; Patent No. 6541458
; GENERAL INFORMATION:
; APPLICANT: Audonnet, et al.
; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V
; FILE REFERENCE: 454313-3151.1
; CURRENT APPLICATION NUMBER: US/09/617,594A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/193,332
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: France 00 01761
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: France 99 09421
; PRIOR FILING DATE: 1999-07-16
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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Felis sp.
US-09-617-594A-10

Query Match 76.2%; Score 578; DB 2; Length 143;
Best Local Similarity 76.9%; Pred. No. 6.7e-61;
Matches 110; Conservative 9; Mismatches 24; Indels 0; Gaps 0;

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Db 1 MWLQNLGTVVYVSMPTPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
Qy 61 SETFDAELTCLQTRKLYKQGRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
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Qy 121 KSFKNLKDFLFEIPFDCWKPAQ 143
Db 121 KNFKNLKDFLFNIPFDCWKPVK 143

RESULT 15
US-10-209-507-10
; Sequence 10, Application US/10209507
; Patent No. 6914134
; GENERAL INFORMATION:
; APPLICANT: Audonnet, et al.
; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V
; FILE REFERENCE: 454313-3151.2
; CURRENT APPLICATION NUMBER: US/10/209,507
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/617,594
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/193,332
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: France 00 01761
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: France 99 09421
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Felis sp.
US-10-209-507-10

Query Match 76.2%; Score 578; DB 2; Length 143;
Best Local Similarity 76.9%; Pred. No. 6.7e-61;
Matches 110; Conservative 9; Mismatches 24; Indels 0; Gaps 0;

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Db 1 MWLQNLGTVVYVSMPTPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
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Qy 121 KSFKNLKDFLFEIPFDCWKPAQ 143
Db 121 KNFKNLKDFLFNIPFDCWKPVK 143

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Job time : 51 secs
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Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	759	100.0	144	5	US-10-614-481-9
2	586	77.2	144	3	US-09-923-246-114
3	586	77.2	144	4	US-10-295-723-114
4	586	77.2	144	4	US-10-282-623-114
5	586	77.2	144	4	US-10-131-985-15
6	586	77.2	144	4	US-10-116-275-217
7	586	77.2	144	4	US-10-456-780-10
8	586	77.2	144	4	US-10-411-037-18
9	586	77.2	144	4	US-10-609-346-20
10	586	77.2	144	4	US-10-411-026-18
11	586	77.2	144	4	US-10-447-315-19
12	586	77.2	144	4	US-10-410-962-18
13	586	77.2	144	4	US-10-411-049-18
14	586	77.2	144	4	US-10-659-684-114
15	586	77.2	144	4	US-10-410-930-18
16	586	77.2	144	4	US-10-410-997-18
17	586	77.2	144	4	US-10-411-012-18
18	586	77.2	144	4	US-10-287-994-18
19	586	77.2	144	4	US-10-659-295-27
20	586	77.2	144	4	US-10-410-913-18
21	586	77.2	144	4	US-10-666-122-3
22	586	77.2	144	4	US-10-666-122-5
23	586	77.2	144	5	US-10-688-845-83
24	586	77.2	144	5	US-10-787-442-114
25	586	77.2	144	5	US-10-901-417-15
26	586	77.2	144	5	US-10-410-980-18
27	586	77.2	144	5	US-10-951-239-8

28	586	77.2	144	5	US-10-410-897-18	Sequence 18, Appl
29	586	77.2	144	5	US-10-492-161-18	Sequence 18, Appl
30	586	77.2	144	5	US-10-880-101A-27	Sequence 27, Appl
31	586	77.2	144	5	US-10-775-204-447	Sequence 447, App
32	586	77.2	144	5	US-10-775-204-448	Sequence 448, App
33	586	77.2	144	5	US-10-775-204-540	Sequence 540, App
34	586	77.2	144	5	US-10-775-204-541	Sequence 541, App
35	586	77.2	144	6	US-11-174-398-10	Sequence 10, Appl
36	586	77.2	144	6	US-11-183-205-18	Sequence 18, Appl
37	586	77.2	610	3	US-09-783-708-1	Sequence 1, Appli
38	586	77.2	729	5	US-10-775-204-324	Sequence 324, App
39	584	76.9	144	4	US-10-081-963-20	Sequence 20, Appl
40	584	76.9	144	4	US-10-351-157-181	Sequence 181, App
41	584	76.9	144	4	US-10-352-554-166	Sequence 166, App
42	584	76.9	144	5	US-10-925-205-6	Sequence 6, Appli
43	584	76.9	144	5	US-10-937-658-3	Sequence 3, Appli
44	584	76.9	144	6	US-11-066-480-6	Sequence 6, Appli
45	584	76.9	144	6	US-11-201-384-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-10-614-481-9  
; Sequence 9, Application US/10614481  
; Publication No. US20050059121A1  
; GENERAL INFORMATION:  
; APPLICANT: Bublot, et al.  
; TITLE OF INVENTION: Equine GM-CSF  
; FILE REFERENCE: 454313-2334.1  
; CURRENT APPLICATION NUMBER: US/10/614,481  
; PRIOR FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: US/09/589,460  
; PRIOR FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: 60/138,843  
; PRIOR FILING DATE: 1999-06-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 9  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Equine sp.  
US-10-614-481-9  
  
Query Match 100.0%; Score 759; DB 5; Length 144;  
Best Local Similarity 100.0%; Pred. No. 3.1e-78;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MWLQNLGTVVYSPAPTRPQHVDAIKEALSLNNSSDTAAIMNETVEV 60  
  
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Db 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGLTMMASHYKQHCPTTETSCATOMITF 120  
  
Qy 121 KSFKNLKDLEFIPDCWKPAQK 144  
Db 121 KSFKNLKDLEFIPDCWKPAQK 144  
  
RESULT 2  
US-09-923-246-114  
; Sequence 114, Application US/09923246  
; Patent No. US20020128446A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020128446A1ak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.



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; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-15

Query Match      77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQHVDAIKALSLLNNSDTAAIMNETVEV 60
DB 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQHVDAIKALSLLNNSDTAAIMNETVEI 60

QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
DB 61 SEMFDLQPTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQIITF 120

QY 121 KSFKKNLKDFLFEPDFCWKPAQ 144
DB 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 6
US-10-116-275-217
; Sequence 217, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 217
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-217

Query Match      77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQHVDAIKALSLLNNSDTAAIMNETVEV 60
DB 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQHVDAIKALSLLNNSDTAAIMNETVEI 60

QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
DB 61 SEMFDLQPTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQIITF 120

QY 121 KSFKKNLKDFLFEPDFCWKPAQ 144
DB 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 7
US-10-456-780-10
; Sequence 10, Application US/10456780
; Publication No. US20040009150A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-780-10

Query Match      77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQHVDAIKALSLLNNSDTAAIMNETVEV 60
DB 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQHVDAIKALSLLNNSDTAAIMNETVEI 60

QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQMITF 120
DB 61 SEMFDLQPTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTTLETSCATQIITF 120

QY 121 KSFKKNLKDFLFEPDFCWKPAQ 144
DB 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 8
US-10-411-037-18
; Sequence 18, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 18
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-411-037-18
Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTLETSCATQIITF 120
QY 121 KSFKKNLKDFLFEIPDCWKPAQK 144
DB 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 9
US-10-609-346-20
; Sequence 20, Application US/10609346
; Publication No. US20040063635A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Zailin
; APPLICANT: Fu, Yan
; TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLOGICAL ACTIVITY
; FILE REFERENCE: ZYU-0603
; CURRENT APPLICATION NUMBER: US/10/609,346
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US 60/392,948
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-609-346-20

Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTLETSCATQIITF 120
QY 121 KSFKKNLKDFLFEIPDCWKPAQK 144
DB 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 10
US-10-411-026-18
; Sequence 18, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakee, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026

US-10-411-037-18
Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTLETSCATQIITF 120
QY 121 KSFKKNLKDFLFEIPDCWKPAQK 144
DB 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 11
US-10-447-315-19
; Sequence 19, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heitsig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-19

Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTLETSCATQIITF 120
QY 121 KSFKKNLKDFLFEIPDCWKPAQK 144
DB 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 12
US-10-447-315-19
; Sequence 19, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heitsig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-19

Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYSPAPTRPSVTRPQWHDVAIKEALSLLNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTLETSCATQIITF 120
QY 121 KSFKKNLKDFLFEIPDCWKPAQK 144
DB 121 ESFKNLKDFLLVIPFDCWEPVQE 144
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Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120
QY 121 KSFKNLKDFLFEIPDCWKPAQ 144
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Db 121 ESFKNLKDFLVIFDCWEPVQE 144

RESULT 12
US-10-410-962-18
; Sequence 18, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-18

Query Match 77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLLLTGVVYMPAPTRPSVTPRWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
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Db 1 MWLQSLLLLTGVVACISAPSPSTQPEWHVNAIQEARLLNLSDRTAAENNETVEVI 60
||||:|||||:||||:|:||||:|:||||:|:||||:|:||||:|:||||:|:
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120
||||:|||||:||||:|:||||:|:||||:|:||||:|:||||:|:||||:|:
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120
||||:|||||:||||:|:||||:|:||||:|:||||:|:||||:|:||||:|:
QY 121 KSFKNLKDFLFEIPDCWKPAQ 144
:||||:|||||:||||:|:
Db 121 ESFKNLKDFLVIFDCWEPVQE 144

RESULT 13
US-10-411-049-18
; Sequence 18, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
```

```
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION: ALPHA
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-049-18

Query Match 77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLLLTGVVYMPAPTRPSVTPRWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
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Db 1 MWLQSLLLLTGVVACISAPSPSTQPEWHVNAIQEARLLNLSDRTAAENNETVEVI 60
||||:|||||:||||:|:||||:|:||||:|:||||:|:||||:|:||||:|:
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120
||||:|||||:||||:|:||||:|:||||:|:||||:|:||||:|:||||:|:
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTSCATQIITF 120
||||:|||||:||||:|:||||:|:||||:|:||||:|:||||:|:||||:|:
QY 121 KSFKNLKDFLFEIPDCWKPAQ 144
:||||:|||||:||||:|:
Db 121 ESFKNLKDFLVIFDCWEPVQE 144

RESULT 14
US-10-659-684-114
; Sequence 114, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
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NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 114  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-659-684-114

Query Match 77.2%; Score 586; DB 4; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.8e-58;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
QY 1 MWLQNLILGTVVYNSMPATPQSPVTRPQWHDVDAIKALSLLNNSDPTAAIMNETVEV 60  
DB 1 MWLQNLILGTVVYNSMPATPQSPVTRPQWHDVDAIKALSLLNNSDPTAAIMNETVEI 60  
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120  
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120  
QY 121 KSFKKNLKDPLFEIPFDCWKPAQK 144  
DB 121 ESFKENLKDPLFLVIPFDCWEPVQE 144

RESULT 15  
US-10-410-930-18  
; Sequence 18, Application US/10410930  
; Publication No. US20040115168A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bowe, Caryn  
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
; FILE OF INVENTION: BETA  
; FILE REFERENCE: 040853-01-5056  
; CURRENT APPLICATION NUMBER: US/10/410,930  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-410-930-18

Query Match 77.2%; Score 586; DB 4; Length 144;  
Best Local Similarity 76.4%; Pred. No. 1.8e-58;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;  
QY 1 MWLQNLILGTVVYNSMPATPQSPVTRPQWHDVDAIKALSLLNNSDPTAAIMNETVEV 60  
DB 1 MWLQNLILGTVVYNSMPATPQSPVTRPQWHDVDAIKALSLLNNSDPTAAIMNETVEI 60  
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120

DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120  
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DB 121 ESFKENLKDPLFLVIPFDCWEPVQE 144  
Search completed: May 25, 2006, 15:16:05  
Job time : 178 secs



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2006, 15:13:17 ; Search time 14 seconds  
(without alignments)  
114.555 Million cell updates/sec

Title: US-10-614-481-9

Perfect score: 759

Sequence: 1 MWLQNLGLGTGVVYVSMPT.....KNLKDPLFEIPDCWKPAQK 144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA\_New.\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586	77.2	144	6	US-10-511-937-2460 Sequence 2460, Ap
2	586	77.2	144	7	US-11-183-218-18 Sequence 18, Appl
3	76	10.0	243	6	US-10-953-349-7275 Sequence 7275, Ap
4	76	10.0	285	6	US-10-953-349-7274 Sequence 7274, Ap
5	76	10.0	363	6	US-10-953-349-7273 Sequence 7273, Ap
6	71.5	9.4	293	6	US-10-953-349-20993 Sequence 20993, A
7	71.5	9.4	382	6	US-10-953-349-20992 Sequence 20992, A
8	70.5	9.3	734	7	US-11-293-697-3300 Sequence 3300, Ap
9	68.5	9.0	129	6	US-10-953-349-15150 Sequence 15150, A
10	68.5	9.0	364	6	US-10-953-349-18543 Sequence 18543, A
11	68.5	9.0	424	6	US-10-953-349-18542 Sequence 18542, A
12	68.5	9.0	438	6	US-10-953-349-18541 Sequence 18541, A
13	68.5	9.0	482	6	US-10-953-349-24953 Sequence 24953, A
14	67.5	8.9	442	6	US-10-953-349-13761 Sequence 13761, A
15	67.5	8.9	445	6	US-10-953-349-13760 Sequence 13760, A
16	67.5	8.9	447	6	US-10-953-349-13759 Sequence 13759, A
17	67	8.8	224	6	US-10-953-349-20916 Sequence 20916, A
18	67	8.8	265	6	US-10-953-349-20915 Sequence 20915, A
19	67	8.8	288	6	US-10-953-349-20914 Sequence 20914, A
20	66	8.7	1089	6	US-10-196-749-266 Sequence 266, App
21	65.5	8.6	202	6	US-10-953-349-27848 Sequence 27848, A
22	65	8.6	337	6	US-10-953-349-10265 Sequence 10265, A
23	64.5	8.5	113	6	US-10-953-349-15151 Sequence 15151, A
24	63.5	8.4	265	7	US-11-314-018-8 Sequence 8, Appl
25	63	8.3	206	6	US-10-196-749-394 Sequence 394, App

#### ALIGNMENTS

##### RESULT 1

US-10-511-937-2460  
; Sequence 2460, Application US/10511937  
; Publication No. US20060088836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2460  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2460

Query Match 77.2%; Score 586; DB 6; Length 144;

Best Local Similarity 76.4%; Pred. No. 5.2e-53;  
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLGLGTGVVYVSMPTQPSPVTRPQVHQVDAIKEALSLLNNSDPTAAIMNETVEV 60

1 MWLQNLGLGTGVVYVSMPTQPSPVTRPQVHQVDAIKEALSLLNNSDPTAAIMNETVEV 60

61 SETPDABELTCLQTRKLYKQGLRSLKLEGPLTMMASHYKQHCPTTLETSCATQMINF 120

61 SEMFDQPTCLQTRKLYKQGLRSLKLEGPLTMMASHYKQHCPTTLETSCATQITTF 120

121 KSFKNLKDPLFEIPDCWKPAQK 144

121 ESFKENLKDPLVLIPDCWEPVQE 144



Query Match  
Best Local Similarity 10.0%; Score 76; DB 6; Length 363;  
Matches 28; Conservative 26; Mismatches 43; Indels 22; Gaps 5;

QY 34 DAKEALSLLNNS-----DTAAIMNETVEVSE--TFDAEELTCLQRLKLYKQ-LR 84  
DB 198 EKIQYMAKMDNTSVENLSPGNVAISSIAKVIASILTYPHEVI-----RAKLOEQGQIR 252

QY 85 GSLIKLEGPLTMMASHYKQHCPTTLETSCATQMTITFKSKQNLKDFLFEI-PFDCWKPAQK 140  
DB 253 NAETKSYGVIDCITKVRSEGIPLGYRGATNLLRTTSPSAVITFYEMWMLRFRQVVP 311

RESULT 6  
US-10-953-349-20993  
; Sequence 20993, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20993  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-20993

Query Match  
Best Local Similarity 9.4%; Score 71.5; DB 6; Length 293;  
Matches 31; Conservative 19; Mismatches 57; Indels 9; Gaps 5;

QY 26 VTRPQHVDIAKEALSLLNNSDTAAIMNETVEVSETFDAEELTCLQRLKLYKQ-LR 84  
DB 76 VLPPYQHGKYGGRFLEVLVDVAISENVDFTVVEEPLDHQVR-TCVDA-LRLLRFGPIQ 133

QY 85 GSLIKLEGPLTMMASHYKQHCPTTLETSCATQMTITFKSKQNLKDFLFEI-PFDCWK 140  
DB 134 NIVTKAVSLLKQEKLSKKAHCPRLLPPPSAIEDVR-KSLKINKQOFL-----QCWE 183

RESULT 7  
US-10-953-349-20992  
; Sequence 20992, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20992  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-20992

Query Match  
Best Local Similarity 9.4%; Score 71.5; DB 6; Length 382;  
Matches 31; Conservative 19; Mismatches 57; Indels 9; Gaps 5;

QY 26 VTRPQHVDIAKEALSLLNNSDTAAIMNETVEVSETFDAEELTCLQRLKLYKQ-LR 84  
DB 165 VLPPYQHGKYGGRFLEVLVDVAISENVDFTVVEEPLDHQVR-TCVDA-LRLLRFGPIQ 222

QY 85 GSLIKLEGPLTMMASHYKQHCPTTLETSCATQMTITFKSKQNLKDFLFEI-PFDCWK 140  
DB 223 NIVTKAVSLLKQEKLSKKAHCPRLLPPPSAIEDVR-KSLKINKQOFL-----QCWE 272

RESULT 8  
US-11-293-697-3300  
; Sequence 3300, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3300  
; LENGTH: 734  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3300

Query Match  
Best Local Similarity 9.3%; Score 70.5; DB 7; Length 734;  
Matches 31; Conservative 13; Mismatches 43; Indels 21; Gaps 5;

QY 38 EALSLLNNSDTAAIMNETVEVSETFDAEELTCLQRLKLYKQGLRSLIKLEGPLTMM 97  
DB 25 EVASLLFDPKAAATIDRDTAFAIGCT-GLEELL-----GIDPSFEQFEAPLFSQ 72

QY 98 ASHYKQHCPTTLETSCATQMTITFKSKQNLKDFLFEI-PFDCWKPAQK 144  
DB 73 LA-----KTLERSVQTKAVN-KOLDENISLFLHLSPYFLKPAQK 112

RESULT 9  
US-10-953-349-15150  
; Sequence 15150, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15150  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-15150

Query Match  
Best Local Similarity 9.0%; Score 68.5; DB 6; Length 129;  
Matches 31; Conservative 17; Mismatches 49; Indels 23; Gaps 7;

QY 6 LLLGL-----TVVYS-----MPAPTRQSPSVTRPQO-HVDAIK-----EALSLLNNSDT 49  
DB 9 LVLLGLNLMVTAHVHGGCGPHCPTTPPPPTSTNGSGSIDTLKLRVCANVLNLLKGLGV 68

QY 50 AAIMNETVEVSETFDAEELTCLQRLKLYKQGLRSLIKLEGSP--LTMASHYKQHCPR 107  
DB 69 PP-SERCCPLADLADLAADVCLTAIRAKVLG-----VIKLVNVPVDLVLNLRHCHTKT 123

RESULT 10  
US-10-953-349-18543  
; Sequence 18543, Application US/10953349

```
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18543
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18543

Query Match          9.0%; Score 68.5; DB 6; Length 364;
Best Local Similarity 22.4%; Pred. No. 8.6;
Matches 35; Conservative 18; Mismatches 40; Indels 63; Gaps 6;

QY 15 SMPAPTRQSPVTRPQWHD-----AIKEALSLLN-----NSSDTAAIMNE 55
Db 138 SSPAPTKKPL-----WOHLSEBALLAKLDPSVAVSYRRALSSRNGLRNTLSRDVRSMSGSS 192
QY 56 TVEVVSSETDAEE-----LTCLOTFLKLYKQGLRGLSLIKLEGPLTMWASHYKQHCPTTL 109
Db 193 PLIFHSSSFSGKNNSLCRLSGTDRIVLYCTSLRG-----IRKTY 233
QY 110 ETSCATQMI-----TFKSFKNLKDPL 131
Db 234 EDCCSVRMLRGFMVAVDERDISMDSSYRKELKDAL 269
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RESULT 11
US-10-953-349-18542
; Sequence 18542, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18542
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18542

Query Match          9.0%; Score 68.5; DB 6; Length 424;
Best Local Similarity 22.4%; Pred. No. 10;
Matches 35; Conservative 18; Mismatches 40; Indels 63; Gaps 6;

QY 15 SMPAPTRQSPVTRPQWHD-----AIKEALSLLN-----NSSDTAAIMNE 55
Db 198 SSPAPTKKPL-----WOHLSEBALLAKLDPSVAVSYRRALSSRNGLRNTLSRDVRSMSGSS 252
QY 56 TVEVVSSETDAEE-----LTCLOTFLKLYKQGLRGLSLIKLEGPLTMWASHYKQHCPTTL 109
Db 253 PLIFHSSSFSGKNNSLCRLSGTDRIVLYCTSLRG-----IRKTY 293
QY 110 ETSCATQMI-----TFKSFKNLKDPL 131
Db 294 EDCCSVRMLRGFMVAVDERDISMDSSYRKELKDAL 329

RESULT 12
US-10-953-349-18541
; Sequence 18541, Application US/109533349
; Publication No. US20060107345A1
```

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; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18541
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18541

Query Match          9.0%; Score 68.5; DB 6; Length 438;
Best Local Similarity 22.4%; Pred. No. 11;
Matches 35; Conservative 18; Mismatches 40; Indels 63; Gaps 6;

QY 15 SMPAPTRQSPVTRPQWHD-----AIKEALSLLN-----NSSDTAAIMNE 55
Db 212 SSPAPTKKPL-----WOHLSEBALLAKLDPSVAVSYRRALSSRNGLRNTLSRDVRSMSGSS 266
QY 56 TVEVVSSETDAEE-----LTCLOTFLKLYKQGLRGLSLIKLEGPLTMWASHYKQHCPTTL 109
Db 267 PLIFHSSSFSGKNNSLCRLSGTDRIVLYCTSLRG-----IRKTY 307
QY 110 ETSCATQMI-----TFKSFKNLKDPL 131
Db 308 EDCCSVRMLRGFMVAVDERDISMDSSYRKELKDAL 343
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RESULT 13
US-10-953-349-24953
; Sequence 24953, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24953
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24953

Query Match          9.0%; Score 68.5; DB 6; Length 482;
Best Local Similarity 30.4%; Pred. No. 12;
Matches 21; Conservative 11; Mismatches 32; Indels 5; Gaps 2;
```

```
QY 44 NNSSDTAAIMNETVEVVSSETDAEELTCLOTFLKLYKQGLRGLSLIKLEGPLTMWASHYKQHCPTTL 98
Db 4 NNSNDAFMRQNAAVQARTKAQNRNVQLKLCQSHPTGLTANLKLFEPRPPEYKYP 63
QY 99 SHYKQHCPTT 107
Db 64 PPEKPKCPP 72

RESULT 14
US-10-953-349-13761
; Sequence 13761, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
```

; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13761  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-13761

Query Match 8.9%; Score 67.5; DB 6; Length 442;  
Best Local Similarity 29.7%; Pred.No.14;  
Matches 22; Conservative 14; Mismatches 27; Indels 11; Gaps 3;  
Qy 46 SSDTAAINNETVEVVSFTDAEELTCLO--TRLKLYKQGLRGLSLIKLEGPLTMMASHYK- 102  
Db 183 SSVAASLVQDITVTLATDPVPAYTFGCIQKATGSSLPQGLLG---LGRGPLSLLAQTQKL 239  
Qy 103 -----QHCPTLET 111  
Db 240 YQSTFSYCLPSPFKT 253

RESULT 15  
US-10-953-349-13760  
; Sequence 13760, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13760  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-13760

Query Match 8.9%; Score 67.5; DB 6; Length 445;  
Best Local Similarity 29.7%; Pred.No.14;  
Matches 22; Conservative 14; Mismatches 27; Indels 11; Gaps 3;  
Qy 46 SSDTAAINNETVEVVSFTDAEELTCLO--TRLKLYKQGLRGLSLIKLEGPLTMMASHYK- 102  
Db 186 SSVAASLVQDITVTLATDPVPAYTFGCIQKATGSSLPQGLLG---LGRGPLSLLAQTQKL 242  
Qy 103 -----QHCPTLET 111  
Db 243 YQSTFSYCLPSPFKT 256

Search completed: May 25, 2006, 15:16:25  
Job time : 14 secs

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